



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 175861**

**TO: Jeanine Goldberg**  
**Location: rem/2D15/2C70**  
**Art Unit: 1634**  
**Tuesday, January 10, 2006**  
**Case Serial Number: 09/954586**

**From: Barb O'Bryen**  
**Location: Biotech-Chem Library**  
**Remsen 1a69**  
**Phone: 571-272-2518** *POB*  
**barbara.obryen@uspto.gov**

### **Search Notes**

# **RUSH**

**This Page Blank (uspto)**

STIC-Biotech/ChemLib

175 861

MEJ

From: Chan, Christina  
Sent: Friday, January 06, 2006 1:23 PM  
To: Goldberg, Jeanine; Fredman, Jeffrey; STIC-Biotech/ChemLib  
Subject: RE: ALLOWANCE AF Search for 09/954586

Please ~~rush~~ Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
JAN - 6 2006  
STIC

-----Original Message-----

From: Goldberg, Jeanine  
Sent: Friday, January 06, 2006 11:44 AM  
To: Chan, Christina; Fredman, Jeffrey  
Subject: ALLOWANCE AF Search for 09/954586

Please search SEQ ID NO: 46 and 59.

THANK YOU!  
Jeanine

Jeanine Anne Goldberg  
1634  
571-272-0743  
REM 2D15  
Mailbox: 2C70

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

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Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 18:14:32 ; Search time 2255 Seconds  
(without alignments)  
579.778 Million cell updates/sec

Title: US-09-954-586-46  
Perfect score: 23  
Sequence: 1 ggataaccgtggtaattcttag 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	23	100.0	23	6	AX421400	AX421400 Sequence
2	23	100.0	23	6	AX421406	AX421406 Sequence
C 3	23	100.0	23	6	AX421412	AX421412 Sequence
C 4	23	100.0	23	6	AX421418	AX421418 Sequence
5	23	100.0	32	6	AX421383	AX421383 Sequence
6	23	100.0	32	6	AX421387	AX421387 Sequence
C 7	23	100.0	32	6	AX421391	AX421391 Sequence
C 8	23	100.0	32	6	AX421395	AX421395 Sequence
9	23	100.0	143	3	AB046950	AB046950 Endophyte
10	23	100.0	144	3	AB046947	AB046947 Endophyte
11	23	100.0	144	3	AB046948	AB046948 Endophyte
12	23	100.0	144	3	AB046949	AB046949 Endophyte
13	23	100.0	145	15	GSU25153	U25153 Glomus sp.
14	23	100.0	145	15	SSU25155	U25155 Scutellospo
15	23	100.0	145	15	SSU25156	U25156 Scutellospo
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31	23	100.0	153	15	AB046941	AB046941 Acaulospo
32	23	100.0	153	15	ASU25151	U25151 Acaulospora
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ALIGNMENTS

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DEFINITION Sequence 46 from Patent WO0222890.  
ACCESSION AX421400  
VERSION AX421400.1 GI:21524795  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.  
TITLE Compositions, methods and kits for determining the presence of cryptosporidium organisms in a test sample  
JOURNAL Patent: WO 0222890-A 46 21-MAR-2002;  
FEATURES Gen-Probe Incorporated (US)  
source Location/Qualifiers  
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DEFINITION Sequence 52 from Patent WO0222890.  
ACCESSION AX421406  
VERSION AX421406.1 GI:21524801  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct

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other sequences; artificial sequences.
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REFERENCE
AUTHORS      Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE        Compositions, methods and kits for determining the presence of
              cryptosporidium organisms in a test sample
JOURNAL      Patent: WO 0222890-A 52 21-MAR-2002;
              Gen-Probe Incorporated (US)
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ACCESSION  AX421412
VERSION     AX421412.1 GI:21524807
KEYWORDS   .
SOURCE     synthetic construct
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           other sequences; artificial sequences.
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REFERENCE
AUTHORS      Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE        Compositions, methods and kits for determining the presence of
              cryptosporidium organisms in a test sample
JOURNAL      Patent: WO 0222890-A 58 21-MAR-2002;
              Gen-Probe Incorporated (US)
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DEFINITION Sequence 64 from Patent WO0222890.
ACCESSION  AX421418
VERSION     AX421418.1 GI:21524813
KEYWORDS   .
SOURCE     synthetic construct
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           other sequences; artificial sequences.
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REFERENCE
AUTHORS      Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE        Compositions, methods and kits for determining the presence of
              cryptosporidium organisms in a test sample
JOURNAL      Patent: WO 0222890-A 64 21-MAR-2002;
              Gen-Probe Incorporated (US)
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VERSION AX421383.1 GI:21524778									
KEYWORDS .									
SOURCE synthetic construct									
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AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.									
TITLE Compositions, methods and kits for determining the presence of									
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Patent: WO 0222890-A 29 21-MAR-2002;									
Gen-Probe Incorporated (US)									
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VERSION AX421387.1 GI:21524782									
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AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.									
TITLE Compositions, methods and kits for determining the presence of									
JOURNAL cryptosporidium organisms in a test sample									
Patent: WO 0222890-A 33 21-MAR-2002;									
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LOCUS AX421391 32 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 37 from Patent WO222890.  
ACCESSION AX421391  
VERSION AX421391.1 GI:21524786  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.  
TITLE Compositions, methods and kits for determining the presence of  
cryptosporidium organisms in a test sample  
JOURNAL Patent: WO 022890-A 37 21-MAR-2002;  
Gen-Probe Incorporated (US)  
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Db 32 GGATAACCGTGGTAATCTAGAG 10

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LOCUS AX421395 32 bp RNA linear PAT 18-JUN-2002  
DEFINITION Sequence 41 from Patent WO0222890.  
ACCESSION AX421395  
VERSION AX421395.1 GI:21524790  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.  
TITLE Compositions, methods and kits for determining the presence of  
cryptosporidium organisms in a test sample  
JOURNAL Patent: WO 022890-A 41 21-MAR-2002;  
Gen-Probe Incorporated (US)  
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/mol\_type="unassigned RNA"  
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Endophyte DG vagiga5 gene for small subunit ribosomal RNA.

ACCESSION AB046950  
VERSION AB046950.1 GI:10039400  
KEYWORDS ENV.  
SOURCE endophyte DG vagiga5  
ORGANISM endophyte DG vagiga5  
Eukaryota; Fungi; Ascomycota; environmental samples.

REFERENCE 1  
AUTHORS Saito,K., Nishiwaki,A. and Sugawara,K.  
TITLE Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNA  
genes from field-collected roots  
JOURNAL Grassl. Sci. 47, 1-8 (2001)  
REFERENCE 2 (bases 1 to 143)  
AUTHORS Saito,K.  
TITLE Direct Submission  
JOURNAL Submitted (04-AUG-2000) Katsuharu Saito, National Institute of  
Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,  
Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp,  
Tel:81-287-37-7691, Fax:81-287-36-6629)  
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AB046947  
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DEFINITION Endophyte DG vagiga2 gene for small subunit ribosomal RNA.  
ACCESSION AB046947  
VERSION AB046947.1 GI:10039397  
KEYWORDS ENV.  
SOURCE endophyte DG vagiga2  
ORGANISM endophyte DG vagiga2  
Eukaryota; Fungi; Ascomycota; environmental samples.

REFERENCE 1  
AUTHORS Saito,K., Nishiwaki,A. and Sugawara,K.  
TITLE Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNA  
genes from field-collected roots  
JOURNAL Grassl. Sci. 47, 1-8 (2001)  
REFERENCE 2 (bases 1 to 144)  
AUTHORS Saito,K.  
TITLE Direct Submission  
JOURNAL Submitted (04-AUG-2000) Katsuharu Saito, National Institute of  
Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,  
Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp,  
Tel:81-287-37-7691, Fax:81-287-36-6629)  
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Db 60 GGATAACCGTGGTAATTCTAGAG 82

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DEFINITION Endophyte DG vagiga3 gene for small subunit ribosomal RNA.  
ACCESSION AB046948  
VERSION AB046948.1 GI:10039398  
KEYWORDS ENV.  
SOURCE endophyte DG vagiga3  
ORGANISM endophyte DG vagiga3  
Eukaryota; Fungi; Ascomycota; environmental samples.

REFERENCE 1  
AUTHORS Saito,K., Nishiwaki,A. and Sugawara,K.  
TITLE Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNA genes from field-collected roots

JOURNAL Grassl. Sci. 47, 1-8 (2001)  
REFERENCE 2 (bases 1 to 144)  
AUTHORS Saito,K.  
TITLE Direct Submission  
JOURNAL Submitted (04-AUG-2000) Katsuharu Saito, National Institute of Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno, Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp, Tel:81-287-37-7691, Fax:81-287-36-6629)

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rRNA

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Db 60 GGATAACCGTGGTAATTCTAGAG 82

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AB046949

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DEFINITION Endophyte DG vagiga4 gene for small subunit ribosomal RNA.  
ACCESSION AB046949  
VERSION AB046949.1 GI:10039399  
KEYWORDS ENV.  
SOURCE endophyte DG vagiga4  
ORGANISM endophyte DG vagiga4  
Eukaryota; Fungi; Ascomycota; environmental samples.

REFERENCE 1  
AUTHORS Saito,K., Nishiwaki,A. and Sugawara,K.  
TITLE Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNA genes from field-collected roots

JOURNAL Grassl. Sci. 47, 1-8 (2001)  
REFERENCE 2 (bases 1 to 144)  
AUTHORS Saito,K.  
TITLE Direct Submission

JOURNAL Submitted (04-AUG-2000) Katsuharu Saito, National Institute of Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno, Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp, Tel:81-287-37-7691, Fax:81-287-36-6629)

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DEFINITION Glomus sp. Glo1 18S ribosomal RNA gene, partial sequence.  
ACCESSION U25153  
VERSION U25153.1 GI:806866  
KEYWORDS .  
SOURCE Glomus sp. Glo1  
ORGANISM Glomus sp. Glo1  
Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;  
Glomeraceae; Glomus.  
1 (bases 1 to 145)  
AUTHORS Clapp,J.P., Young,J.W., Merryweather,J.W. and Pitter,A.H.  
TITLE Diversity of fungal symbionts in arbuscular mycorrhizas from a natural community

JOURNAL New Phytol. 130 (2), 259-265 (1995)  
REFERENCE 2 (bases 1 to 145)  
AUTHORS Clapp,J.P.  
TITLE Direct Submission  
JOURNAL Submitted (18-APR-1995) Justin P. Clapp, Biology, University of York, Heslington, York, North Yorkshire YO1 5YW, England

FEATURES  
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rRNA

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Db 60 GGATAACCGTGGTAATTCTAGAG 82

RESULT 14  
SSU25155



LOCUS	SSU25155	145 bp	DNA	linear	PLN 22-JAN-2003
DEFINITION	Scutellospora sp. scut2 18S ribosomal RNA gene, partial sequence.				
ACCESSION	U25155				
VERSION	U25155.1	GI:806868			
KEYWORDS					
SOURCE	Scutellospora sp. Scut2				
ORGANISM	Scutellospora sp. Scut2				
	Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Diversisporales; Gigasporaceae; Scutellospora.				
REFERENCE	1 (bases 1 to 145)				
AUTHORS	Clapp,J.P., Young,J.W., Merryweather,J.W. and Fitter,A.H.				
TITLE	Diversity of fungal symbionts in arbuscular mycorrhizas from a natural community				
JOURNAL	New Phytol. 130 (2), 259-265 (1995)				
REFERENCE	2 (bases 1 to 145)				
AUTHORS	Clapp,J.P.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-APR-1995) Justin P. Clapp, Biology, University of York, Heslington, York, North Yorkshire YO1 5YW, England				
FEATURES	Location/Qualifiers				
source	1..145				
	/organism="Scutellospora sp. Scut2"				
	/mol_type="genomic DNA"				
	/specific_host="Hyacinthoides non-scripta"				
	/db_xref="taxon:39837"				
	/clone="scut2"				
	/tissue_type="intraradical hyphae"				
rRNA	<1..>145				
	/product="18S ribosomal RNA"				
	/note="corresponds to bases 83-277 of the 18S ribosomal RNA gene of Saccharomyces cerevisiae, GenBank Accession Number J01353"				
ORIGIN					
	Query Match 100.0%; Score 23; DB 15; Length 145;				
	Best Local Similarity 100.0%; Pred. No. 1.1;				
	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GGATAACCGTGGTAATTCTAGAG 23				
Db	61 GGATAACCGTGGTAATTCTAGAG 83				
RESULT 15					
SSU25156					
LOCUS	SSU25156	145 bp	DNA	linear	PLN 22-JAN-2003
DEFINITION	Scutellospora sp. scut1 18S ribosomal RNA gene, partial sequence.				
ACCESSION	U25156				
VERSION	U25156.1	GI:806869			
KEYWORDS					
SOURCE	Scutellospora sp. Scut1				
ORGANISM	Scutellospora sp. Scut1				
	Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Diversisporales; Gigasporaceae; Scutellospora.				
REFERENCE	1 (bases 1 to 145)				
AUTHORS	Clapp,J.P., Young,J.W., Merryweather,J.W. and Fitter,A.H.				
TITLE	Diversity of fungal symbionts in arbuscular mycorrhizas from a natural community				
JOURNAL	New Phytol. 130 (2), 259-265 (1995)				
REFERENCE	2 (bases 1 to 145)				
AUTHORS	Clapp,J.P.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-APR-1995) Justin P. Clapp, Biology, University of York, Heslington, York, North Yorkshire YO1 5YW, England				
FEATURES	Location/Qualifiers				
source	1..145				
	/organism="Scutellospora sp. Scut1"				
	/mol_type="genomic DNA"				
	/specific_host="Hyacinthoides non-scripta"				
	/db_xref="taxon:108482"				
	/clone="scut1"				
	/tissue_type="intraradical hyphae"				
rRNA	<1..>145				

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 16:34:41 ; Search time 327 Seconds  
(without alignments)  
468.770 Million cell updates/sec

Title: US-09-954-586-46  
Perfect score: 23  
Sequence: 1 ggataaccgtggttaattctag 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	6	AAD38426
2	23	100.0	23	6	AAD38438
3	23	100.0	23	6	AAD38444
4	23	100.0	23	6	AAD38432
5	23	100.0	32	6	AAD38409
6	23	100.0	32	6	AAD38421
7	23	100.0	32	6	AAD38413
8	23	100.0	32	6	AAD38417
9	23	100.0	384	14	ADY98693
10	23	100.0	444	2	AAQ71869
11	23	100.0	447	2	AAQ71867
12	23	100.0	447	2	AAQ71870
13	23	100.0	447	2	AAQ71868
14	23	100.0	488	13	ADR99351
15	23	100.0	501	6	ABS53676
16	23	100.0	538	14	ADY98694
17	23	100.0	540	14	ADY98695
18	23	100.0	570	3	AAF08498
19	23	100.0	570	13	ADU52539

c	20	23	100.0	570	14	ADZ90542	Adz90542 Fusarium
	21	23	100.0	617	3	AAF10913	Aaf10913 Fusarium
	22	23	100.0	617	13	ADU54954	Adu54954 Fusarium
	23	23	100.0	617	14	ADZ92957	Adz92957 Fusarium
	24	23	100.0	1228	10	ABZ80030	Abz80030 Xylariale
	25	23	100.0	1247	10	ACA61067	Aca61067 Phyllosti
	26	23	100.0	1727	6	ABV78726	Abv78726 C. sinens
	27	23	100.0	1731	4	AAI68286	Aai68286 Bulgaria
	28	23	100.0	1731	6	ABA01154	Aba01154 Deuteromy
	29	23	100.0	1731	13	ADP79725	Adp79725 Anti-tumo
	30	23	100.0	1732	12	ADH43081	Adh43081 18s rRNA
	31	23	100.0	1733	13	ADP79724	Adp79724 Anti-tumo
	32	23	100.0	1743	11	ADZ11854	Adz11854 Geotrichu
	33	23	100.0	1745	6	ABA01152	Aba01152 Deuteromy
	34	23	100.0	1750	2	AAT90818	Aat90818 C. parvum
	35	23	100.0	1750	3	AAA46368	Aaa46368 Nucleotid
	36	23	100.0	1761	6	ABV78699	Abv78699 C. crassi
	37	23	100.0	1766	6	ABV78720	Abv78720 C. sinens
	38	23	100.0	1766	6	ABV78708	Abv78708 C. sinens
	39	23	100.0	1766	6	ABV78714	Abv78714 C. sinens
	40	23	100.0	1766	6	ABV78711	Abv78711 C. sinens
	41	23	100.0	1766	6	ABV78717	Abv78717 C. sinens
	42	23	100.0	1766	6	ABV78705	Abv78705 C. sinens
	43	23	100.0	1766	6	ABV78702	Abv78702 C. sinens
	44	23	100.0	1766	6	ABV78723	Abv78723 C. sinens
	45	23	100.0	1771	2	AAV61668	Aav61668 Fusarium

ALIGNMENTS

RESULT 1  
AAD38426  
ID AAD38426 standard; DNA; 23 BP.  
XX  
AC AAD38426;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Cryptosporidium sp. target DNA #8.  
XX  
KW Hybridisation; amplification; detection; ds.  
XX  
OS Cryptosporidium sp.  
XX  
PN WO200222890-A2.  
XX  
PD 21-MAR-2002.  
XX  
PF 11-SEP-2001; 2001WO-US042192.  
XX  
PR 12-SEP-2000; 2000US-0232028P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Cunningham MM, Stull PD, Weisburg WG;  
XX  
DR WPI; 2002-454395/48.  
XX  
PT Novel oligonucleotides functioning as hybridization probes, helper probes and/or primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms, useful for detecting the organism in a test sample.  
XX  
PS Claim 23; Page 8; 133pp; English.  
XX  
CC The invention relates to oligonucleotides functioning as hybridisation assay probes, helper probes and/or amplification primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms. Probes and primers of the invention are useful for detecting the presence of Cryptosporidium organisms in general and C. parvum organisms in particular in a test sample. The present sequence is Cryptosporidium sp. target DNA



DR WPI; 2002-454395/48.

XX Novel oligonucleotides functioning as hybridization probes, helper probes

PT and/or primers, targeted to nucleic acid sequences derived from

PT Cryptosporidium organisms, useful for detecting the organism in a test

PT sample.

XX

PS Claim 23; Page 8; 133pp; English.

XX

CC The invention relates to oligonucleotides functioning as hybridisation

CC assay probes, helper probes and/or amplification primers, targeted to

CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and

CC primers of the invention are useful for detecting the presence of

CC Cryptosporidium organisms in general and C. parvum organisms in

CC particular in a test sample. The present sequence is Cryptosporidium sp.

CC target RNA

XX

SQ Sequence 23 BP; 7 A; 3 C; 7 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 23;

Best Local Similarity 73.9%; Pred. No. 0.18;

Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23

Db 1 GGAUAACCGUGGUAUUCUAGAG 23

RESULT 5

AAD38409

ID AAD38409 standard; DNA; 32 BP.

XX

AC AAD38409;

XX

DT 10-SEP-2002 (first entry)

XX

DE Cryptosporidium parvum target DNA #9.

XX

XX Hybridisation; amplification; detection; ds.

OS Cryptosporidium parvum.

XX

XX WO200222890-A2.

PN

XX

PD 21-MAR-2002.

XX

PF 11-SEP-2001; 2001WO-US042192.

XX

XX 12-SEP-2000; 2000US-0232028P.

PR

XX (GENP-) GEN-PROBE INC.

PA

XX

PI Cunningham MM, Stull PD, Weisburg WG;

XX

DR WPI; 2002-454395/48.

XX

XX Novel oligonucleotides functioning as hybridization probes, helper probes

PT and/or primers, targeted to nucleic acid sequences derived from

PT Cryptosporidium organisms, useful for detecting the organism in a test

PT sample.

XX

PS Claim 102; Page 6; 133pp; English.

XX

CC The invention relates to oligonucleotides functioning as hybridisation

CC assay probes, helper probes and/or amplification primers, targeted to

CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and

CC primers of the invention are useful for detecting the presence of

CC Cryptosporidium organisms in general and C. parvum organisms in

CC particular in a test sample. The present sequence is C. parvum target DNA

XX

SQ Sequence 32 BP; 11 A; 5 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 32;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23

Db 1 GGATAACCGTGGTAATTCTAGAG 23

RESULT 6

AAD38421/c

ID AAD38421 standard; RNA; 32 BP.

XX

AC AAD38421;

XX

DT 10-SEP-2002 (first entry)

XX

DE Cryptosporidium parvum target RNA #13.

XX

KW Hybridisation; amplification; detection; ss.

XX

OS Cryptosporidium parvum.

XX

PN WO200222890-A2.

XX

PD 21-MAR-2002.

XX

PF 11-SEP-2001; 2001WO-US042192.

XX

PR 12-SEP-2000; 2000US-0232028P.

XX

PA (GENP-) GEN-PROBE INC.

XX

PI Cunningham MM, Stull PD, Weisburg WG;

XX

DR WPI; 2002-454395/48.

XX

PT Novel oligonucleotides functioning as hybridization probes, helper probes

PT and/or primers, targeted to nucleic acid sequences derived from

PT Cryptosporidium organisms, useful for detecting the organism in a test

PT sample.

XX

PS Claim 102; Page 6; 133pp; English.

XX

CC The invention relates to oligonucleotides functioning as hybridisation

CC assay probes, helper probes and/or amplification primers, targeted to

CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and

CC primers of the invention are useful for detecting the presence of

CC Cryptosporidium organisms in general and C. parvum organisms in

CC particular in a test sample. The present sequence is C. parvum target RNA.

XX

SQ Sequence 32 BP; 9 A; 7 C; 5 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 32;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23

Db 32 GGATAACCGTGGTAATTCTAGAG 10

RESULT 7

AAD38413

ID AAD38413 standard; RNA; 32 BP.

XX

AC AAD38413;

XX

DT 10-SEP-2002 (first entry)

XX

DE Cryptosporidium parvum target RNA #9.

XX

KW Hybridisation; amplification; detection; ss.

XX

OS Cryptosporidium parvum.  
XX  
PN WO200222890-A2.  
XX  
PD 21-MAR-2002.  
XX  
PF 11-SEP-2001; 2001WO-US042192.  
XX  
PR 12-SEP-2000; 2000US-0232028P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Cunningham MM, Stull PD, Weisburg WG;  
XX  
DR WPI; 2002-454395/48.  
XX  
PT Novel oligonucleotides functioning as hybridization probes, helper probes  
and/or primers, targeted to nucleic acid sequences derived from  
PT Cryptosporidium organisms, useful for detecting the organism in a test  
PT sample.  
XX  
PS Claim 102; Page 6; 133pp; English.  
XX  
CC The invention relates to oligonucleotides functioning as hybridisation  
assay probes, helper probes and/or amplification primers, targeted to  
CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and  
CC primers of the invention are useful for detecting the presence of  
CC Cryptosporidium organisms in general and C. parvum organisms in  
CC particular in a test sample. The present sequence is C. parvum target RNA  
XX  
SQ Sequence 32 BP; 11 A; 5 C; 7 G; 0 T; 9 U; 0 Other;  
  
Query Match 100.0%; Score 23; DB 6; Length 32;  
Best Local Similarity 73.9%; Pred. No. 0.19;  
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||:|||||:|:|:|:|:|:  
Db 1 GGAUAACCGUGGUAUUCUAGAG 23  
  
RESULT 8  
AAD38417/c  
ID AAD38417 standard; DNA; 32 BP.  
XX  
AC AAD38417;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Cryptosporidium parvum target DNA #13.  
XX  
KW Hybridisation; amplification; detection; ds.  
XX  
OS Cryptosporidium parvum.  
XX  
PN WO200222890-A2.  
XX  
PD 21-MAR-2002.  
XX  
PF 11-SEP-2001; 2001WO-US042192.  
XX  
PR 12-SEP-2000; 2000US-0232028P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Cunningham MM, Stull PD, Weisburg WG;  
XX  
DR WPI; 2002-454395/48.  
XX  
PT Novel oligonucleotides functioning as hybridization probes, helper probes  
and/or primers, targeted to nucleic acid sequences derived from  
PT Cryptosporidium organisms, useful for detecting the organism in a test  
PT sample.

XX Claim 102; Page 6; 133pp; English.  
PS  
XX  
CC The invention relates to oligonucleotides functioning as hybridisation  
assay probes, helper probes and/or amplification primers, targeted to  
CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and  
CC primers of the invention are useful for detecting the presence of  
CC Cryptosporidium organisms in general and C. parvum organisms in  
CC particular in a test sample. The present sequence is C. parvum target DNA  
XX  
SQ Sequence 32 BP; 9 A; 7 C; 5 G; 11 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 23; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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|||:|||||:|:|:|:|:|:  
Db 32 GGATAACCGTGGTAATTCTAGAG 10  
  
RESULT 9  
ADY98693/c  
ID ADY98693 standard; CDNA; 384 BP.  
XX  
AC ADY98693;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE T\_reesei suppressive subtractive hybridization (SSH) cDNA clone Seq 47.  
XX  
KW gene expression; suppressive subtractive hybridization; microarray;  
KW microorganism; ss.  
XX  
OS Hypocrea jecorina.  
XX  
PN US2005069934-A1.  
XX  
PD 31-MAR-2005.  
XX  
PF 24-SEP-2004; 2004US-00950009.  
XX  
PR 25-SEP-2003; 2003US-0506140P.  
XX  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
XX  
PI Berka R, Bashkirova E, Rey M;  
XX  
DR WPI; 2005-271963/28.  
XX  
PT Monitoring differential expression of genes of two filamentous fungal  
cells, for e.g. discovering new genes, comprises adding labeled nucleic  
PT acids to an array of Trichoderma reesei expressed sequenced tags and  
PT detecting spots.  
XX  
PS Claim 1; SEQ ID NO 47; 27pp; English.  
XX  
CC This invention relates to a novel method for monitoring differential  
expression of genes in a filamentous fungal cell. Specifically, it refers  
CC to identifying differential gene expression occurring between two related  
CC filamentous fungal cells and comprises adding detection reporter labeled  
CC nucleic acids of filamentous fungal cells to a substrate array of  
CC Trichoderma reesei (T. reesei) expressed sequenced tags (ESTs), or  
CC suppression subtractive hybridization (SSH) clones and detecting a signal  
CC in the array. The present invention further describes a computer readable  
CC medium having for monitoring differential expression of several genes in  
CC a first filamentous fungal cell relative to expression of the same genes  
CC in one or more second filamentous fungal cells. It also provides a search  
CC unit for comparing a target sequence to a T. reesei EST sequence of the  
CC data storage unit to identify homologous sequences, and a retrieval unit  
CC for obtaining the homologous sequence(s). Accordingly, it provides a  
CC method useful for identifying microbial genes induced when the  
CC microorganism is grown on cellulose or corn stover, as well as for



CC discovering new genes, identifying possible functions of unknown open  
CC reading frames and monitoring gene copy number variation and stability.  
CC Note that this method utilizes an array where one spot equals one gene or  
CC open reading frame, which makes extensive follow-up characterization  
CC unnecessary since sequence information is available and EST and/or SSH  
CC microarrays can be organized based on function of the gene products. This  
CC polynucleotide sequence is a T. reesei SSH cDNA clone that forms part of  
CC the substrate array of the invention. NOTE: The SeqIDs 1-1188 referring  
CC to T. reesei ESTs or SSH clones or their combinations are available in  
CC electronic form from the USPTO web site  
CC (<http://seqdata.uspto.gov/sequence.html>; Document ID:20050069934).  
XX  
SQ Sequence 384 BP; 108 A; 83 C; 88 G; 105 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 14; Length 384;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23  
|||||  
Db 234 GGATAACCGTGGTAATTCCTAGAG 212

RESULT 10  
AAQ71869  
ID AAQ71869 standard; DNA; 444 BP.  
XX  
AC AAQ71869;  
XX  
DT 23-MAR-1995 (first entry)  
XX  
DE G. margarita small ribosomal subunit RNA.  
XX  
KW Nuclear 18S ribosomal gene; SSU; probe; primer;  
KW arbuscular endomycorrhizal fungi; plant; root; ds.  
XX  
OS Gigaspora margarita.  
XX  
PN CA2086136-A.  
XX  
PD 24-JUN-1994.  
XX  
PF 23-DEC-1992; 92CA-02086136.  
XX  
PR 23-DEC-1992; 92CA-02086136.  
XX

(SIMO/) SIMON L.

Simon L, Lalonde M;  
WPI; 1994-264577/33.

New oligonucleotide probes - used for the detection of arbuscular  
endomycorrhizal fungi in plant root samples.

Disclosure; Page 19; 40pp; English.

The gene sequence of the small ribosomal subunit RNA of arbuscular  
endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus  
intraradices and Gigaspora margarita were compared with that of a non-  
arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to  
design taxon specific primers/probes

Sequence 444 BP; 134 A; 81 C; 104 G; 125 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 2; Length 444;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23  
|||||  
Db 33 GGATAACCGTGGTAATTCCTAGAG 55

RESULT 11  
AAQ71867  
ID AAQ71867 standard; DNA; 447 BP.  
XX  
AC AAQ71867;  
XX  
DT 23-MAR-1995 (first entry)  
XX  
DE G. vesiculiferum small ribosomal subunit RNA.  
XX  
KW Nuclear 18S ribosomal gene; SSU; probe; primer;  
KW arbuscular endomycorrhizal fungi; plant; root; ds.  
XX

Glomus vesiculiferum.

CA2086136-A.

24-JUN-1994.

23-DEC-1992; 92CA-02086136.

23-DEC-1992; 92CA-02086136.

(SIMO/) SIMON L.

Simon L, Lalonde M;

WPI; 1994-264577/33.

New oligonucleotide probes - used for the detection of arbuscular  
endomycorrhizal fungi in plant root samples.

Disclosure; Page 18; 40pp; English.

The gene sequence of the small ribosomal subunit RNA of arbuscular  
endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus  
intraradices and Gigaspora margarita were compared with that of a non-  
arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to  
design taxon specific primers/probes

Sequence 447 BP; 135 A; 86 C; 107 G; 118 T; 0 U; 1 Other;

Query Match 100.0%; Score 23; DB 2; Length 447;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23  
|||||  
Db 32 GGATAACCGTGGTAATTCCTAGAG 54

RESULT 12

AAQ71870

ID AAQ71870 standard; DNA; 447 BP.

XX  
AC AAQ71870;

DT 23-MAR-1995 (first entry)

XX E. pisiformis small ribosomal subunit RNA.

Nuclear 18S ribosomal gene; SSU; probe; primer;

arbuscular endomycorrhizal fungi; plant; root; ds.

XX Endogone pisiformis.

OS

Key Location/Qualifiers

FT misc\_difference 116.135

FT /\*tag= a

FT /note= "bases not determined"

XX CA2086136-A.

PN



XX PD 24-JUN-1994.

XX PF 23-DEC-1992; 92CA-02086136.

XX PR 23-DEC-1992; 92CA-02086136.

XX PA (SIMO/) SIMON L.

XX PI Simon L, Lalonde M;

XX DR WPI; 1994-264577/33.

XX PT New oligonucleotide probes - used for the detection of arbuscular

XX PT endomycorrhizal fungi in plant root samples.

XX PS Disclosure; Page 20; 40pp; English.

XX CC The gene sequence of the small ribosomal subunit RNA of arbuscular

XX CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus

XX CC intraradices and Gigaspora margarita were compared with that of a non-

XX CC arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to

XX CC design taxon specific primers/probes

SQ Sequence 447 BP; 133 A; 77 C; 100 G; 117 T; 0 U; 20 Other;

Query Match 100.0%; Score 23; DB 2; Length 447;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23

Db 33 GGATAACCGTGGTAATTCTAGAG 55

RESULT 13

AAQ71868

ID AAQ71868 standard; DNA; 447 BP.

XX AC AAQ71868;

XX DT 23-MAR-1995 (first entry)

XX DE G. intraradices small ribosomal subunit RNA.

XX KW Nuclear 18S ribosomal gene; SSU; probe; primer;

XX KW arbuscular endomycorrhizal fungi; plant; root; ds.

XX OS Glomus intraradices.

XX PN CA2086136-A.

XX PD 24-JUN-1994.

XX PF 23-DEC-1992; 92CA-02086136.

XX PR 23-DEC-1992; 92CA-02086136.

XX PA (SIMO/) SIMON L.

XX PI Simon L, Lalonde M;

XX DR WPI; 1994-264577/33.

XX PT New oligonucleotide probes - used for the detection of arbuscular

XX PT endomycorrhizal fungi in plant root samples.

XX PS Disclosure; Page 19; 40pp; English.

XX CC The gene sequence of the small ribosomal subunit RNA of arbuscular

XX CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus

XX CC intraradices and Gigaspora margarita were compared with that of a non-

XX CC arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to

CC design taxon specific primers/probes

XX SQ Sequence 447 BP; 137 A; 86 C; 107 G; 117 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 2; Length 447;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23

Db 32 GGATAACCGTGGTAATTCTAGAG 54

RESULT 14

ADR99351

ID ADR99351 standard; DNA; 488 BP.

XX AC ADR99351;

XX DT 16-DEC-2004 (first entry)

XX DE Acremonium 18S rDNA gene sequence.

XX KW algicide; red tide; dinoflagellate; 18S rDNA gene; ds.

XX OS Acremonium sp.

XX PN JP2004262879-A.

XX PD 24-SEP-2004.

XX PF 04-MAR-2003; 2003JP-00056623.

XX PR 04-MAR-2003; 2003JP-00056623.

XX PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.

XX DR WPI; 2004-672306/66.

XX PT Novel cyclic peptide, useful as algicide for exterminating red tide

XX PT containing dinoflagellates in seas, lakes, marshes, seashores, artificial

XX PS Disclosure; SEQ ID NO 1; 18pp; Japanese.

XX CC The invention comprises a cyclic peptide which has algicide activity

XX CC against red tide containing dinoflagellates, without exerting any

XX CC influence on the environment. The cyclic peptide of the invention is

XX CC useful as an algicide for exterminating red tide containing

XX CC dinoflagellates belonging to Protocentrum, Heterocapsa and Gymnodinium

XX CC sp. in seas, lakes, marshes, seashores, artificial ponds and pools. The

XX CC present DNA sequence represents an Acremonium 18S rDNA gene sequence that

XX CC was used in the exemplification of the invention.

XX SQ Sequence 488 BP; 138 A; 100 C; 117 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 13; Length 488;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23

Db 71 GGATAACCGTGGTAATTCTAGAG 93

RESULT 15

ABS53676

ID ABS53676 standard; DNA; 501 BP.

XX AC ABS53676;

XX DT 20-NOV-2002 (first entry)

DE Filamentous fungi 18S rDNA partial sequence.  
XX  
KW Antimicrobial agent; slime; PCR; primer; ss; papermaking industry;  
KW 18S rDNA; filamentous fungi.  
XX  
OS Ascomycota.  
XX  
PN WO200254865-A1.  
XX  
PD 18-JUL-2002.  
XX  
PF 08-JAN-2002; 2002WO-JP0000012.  
XX  
PR 09-JAN-2001; 2001JP-00001427.  
PR 10-JUL-2001; 2001JP-00209845.  
PR 29-NOV-2001; 2001JP-00365004.  
XX  
PA (KURK ) KURITA WATER IND LTD.  
XX  
PI Iizumi T, Suzuki H, Tashiro H;  
XX  
DR WPI; 2002-682647/73.  
XX  
PT New method, useful in screening anti-microbial agents for controlling  
PT slimes in papermaking industry or monitoring anti-microbial effect,  
PT comprises microbial analysis step and anti-microbial selection step.  
XX  
PS Example 10; Page 91-92; 94pp; Japanese.  
XX  
CC The invention relates to a method for selecting an anti-microbial agent,  
CC comprising: (A) the microbial analysis step of analysing the microbial  
CC phase of a sample based on DNA base sequences (e.g. by PCR); and (B) the  
CC anti-microbial selection step by searching a database for matching and  
CC extracting an industrial anti-microbial agent with optimum anti-microbial  
CC properties. The method may be used to choose anti- microbial agents for  
CC treatment of microorganism-containing samples, to monitor the effect of  
CC added antimicrobial agent over time in a sample or process, to inhibit or  
CC regulate slime in paper manufacturing and for the analysis of adherent on  
CC paper products during manufacture, in which DNAs are extracted from the  
CC adherent-causing microorganisms for analysis to reveal the microbial  
CC phase or predominant or specific microorganism, e.g. slime, after  
CC comparison. The method is used for screening and selecting anti-microbial  
CC agents particularly for controlling and treating slimes in papermaking  
CC industry, which can also be applied in monitoring anti-microbial effect,  
CC analysis of product adherents. The present sequence is a Filamentous  
CC fungi 18S rDNA partial sequence isolated by the method of the invention  
XX  
SQ Sequence 501 BP; 146 A; 100 C; 122 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 501;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||  
Db 98 GGATAACCGTGGTAATTCTAGAG 120  
|||

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 18:15:11 ; Search time 2474 Seconds  
(without alignments)  
434.965 Million cell updates/sec

Title: US-09-954-586-46  
Perfect score: 23  
Sequence: 1 ggataaccgtgtaattctag 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_htc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	154	1 AU012137	AU012137 AU012137
2	23	100.0	154	1 AU012452	AU012452 AU012452
3	23	100.0	191	1 AW217889	AW217889 EST296603
4	23	100.0	193	1 AU006980	AU006980 AU006980
5	23	100.0	200	1 AU009944	AU009944 AU009944
6	23	100.0	208	1 AU010607	AU010607 AU010607
7	23	100.0	216	1 AL749833	AL749833 AL749833
8	23	100.0	222	1 AW791051	AW791051 D00369-R
9	23	100.0	230	7 CF945579	CF945579 TrEST-A28
10	23	100.0	233	7 CF945596	CF945596 TrEST-A28
11	23	100.0	236	7 CF945185	CF945185 TrEST-A28
12	23	100.0	254	1 AA532319	AA532319 CpEST.449
13	23	100.0	256	6 CD029939	CD029939 mgmk014xB
14	23	100.0	269	1 AI398053	AI398053 NCSC2C4T7
15	23	100.0	278	5 BU638475	BU638475 mgcw009xE
16	23	100.0	290	7 CF945670	CF945670 TrEST-A35
17	23	100.0	294	5 BU644435	BU644435 mgmk020xN
18	23	100.0	295	2 BE358258	BE358258 DG1 27 B0
19	23	100.0	295	7 CF945416	CF945416 TrEST-A32
20	23	100.0	303	2 BE125593	BE125593 DG1 28 G0
21	23	100.0	303	7 CF945202	CF945202 TrEST-A10
22	23	100.0	323	5 BU640864	BU640864 mgmk003xK

23	100.0	329	7	CF945598	CF945598 TrEST-A07
24	100.0	336	5	BU644444	BU644444 mgmk020xP
25	100.0	345	7	CN797076	CN797076 DK8P00770
26	100.0	354	6	CD456115	CD456115 Fg03 07g0
27	100.0	355	6	CD460057	CD460057 Fg09_0802
28	100.0	363	7	CK907640	CK907640 rhzma0 00
29	100.0	375	7	CF945482	CF945482 TrEST-A40
30	100.0	376	11	CNS06X4Z	AL419289 T7 end of
31	100.0	377	1	AW332754	AW332754 S12E8 AGS
32	100.0	396	2	BE358268	BE358268 DG1 27 A0
33	100.0	397	7	CF945055	CF945055 TrEST-A24
34	100.0	400	6	CD036436	CD036436 mgmt020xA
35	100.0	405	1	AJ638699	AJ638699 AJ638699
36	100.0	410	6	CA683922	CA683922 wlm96.pk0
37	100.0	410	7	CF945824	CF945824 TrEST-A00
38	100.0	412	7	CF945285	CF945285 TrEST-A24
39	100.0	413	7	CF945742	CF945742 TrEST-A31
40	100.0	414	7	CF945319	CF945319 TrEST-A06
41	100.0	417	1	AW333127	AW333127 S17F5 AGS
42	100.0	419	7	CN799791	CN799791 DI8P01632
43	100.0	421	7	CN749598	CN749598 APAL3SD-X
44	100.0	426	2	BE710613	BE710613 QV3-HT063
45	100.0	426	7	CF945631	CF945631 TrEST-A26

ALIGNMENTS

RESULT 1  
AU012137 154 bp mRNA linear EST 03-AUG-1998  
LOCUS AU012137 Schizosaccharomyces pombe late log phase cDNA  
DEFINITION Schizosaccharomyces pombe cDNA clone spc06398, mRNA sequence.  
ACCESSION AU012137  
VERSION AU012137.1 GI:3357046  
KEYWORDS EST.  
SOURCE Schizosaccharomyces pombe (fission yeast)  
ORGANISM Schizosaccharomyces pombe  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomycetes.  
REFERENCE 1 (bases 1 to 154)  
AUTHORS Morimyo,M. and Mita,K.  
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe  
JOURNAL Unpublished (1998)  
COMMENT Contact: Mitsuoki Morimyo  
Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: morimyo@nirs.go.jp.

FEATURES  
source Location/Qualifiers  
1..154  
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/mol\_type="mRNA"  
/strain="972"  
/db\_xref="taxon:4896"  
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/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN  
Query Match 100.0%; Score 23; DB 1; Length 154;  
Best Local Similarity 100.0%; Pred. No. 0.6;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGATAACCGTGGTAATTCTAGAG 23

Db		87	GGATAACCGTGGTAATTCTAGAG	109		JOURNAL COMMENT	Unpublished (1999) Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> 5 prime sequence.
RESULT 2							
AU012452							
LOCUS			154 bp	mRNA	linear	EST 03-AUG-1998	
DEFINITION			AU012452 Schizosaccharomyces pombe	cdna	late log phase	cdna	
ACCESSION			Schizosaccharomyces pombe	cdna	clone spc06817,	mRNA	sequence.
VERSION			AU012452				
KEYWORDS			AU012452.1	GI:3357361			
SOURCE			EST.				
ORGANISM			Schizosaccharomyces pombe	(fission yeast)			
			Schizosaccharomyces pombe				
			Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;				
			Schizosaccharomycetales; Schizosaccharomycetaceae;				
			Schizosaccharomyces.				
REFERENCE			1 (bases 1 to 154)				
AUTHORS			Morimyo,M. and Mita,K.				
TITLE			Identification of expressed sequence tags of Schizosaccharomyces				
JOURNAL COMMENT			pombe				
			Unpublished (1998)				
			Contact: Mitsuoki Morimyo				
			Genome Research Group				
			National Institute of Radiological Sciences				
			9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan				
			Email: <a href="mailto:morimyo@nirs.go.jp">morimyo@nirs.go.jp</a> .				
FEATURES			Location/Qualifiers				
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			into the SmaI site of M13mp19 DNA and the direction of DNA				
			sequences was not always from 5' to 3'. The cdna data of				
			Schizosaccharomyces pombe are available for searching on				
			the World Wide Web. (URL, <a href="http://www.nirs.go.jp">http://www.nirs.go.jp</a> )"				
ORIGIN							
			Query Match	100.0%;	Score 23;	DB 1;	Length 154;
			Best Local Similarity	100.0%;	Pred. No. 0.6;		
			Matches	23;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY			1	GGATAACCGTGGTAATTCTAGAG	23		
Db							
			87	GGATAACCGTGGTAATTCTAGAG	109		
RESULT 3							
AW217889							
LOCUS			191 bp	mRNA	linear	EST 18-MAY-2001	
DEFINITION			AW217889 tomato flower buds, anthesis, Cornell University				
			Lycopersicon esculentum cdna	clone ctOD1C1	similar to	Ipomoea	
			hederacea 18S ribosomal RNA gene, mRNA	sequence.			
ACCESSION			AW217889				
VERSION			AW217889.1	GI:6528763			
KEYWORDS			EST.				
SOURCE			Lycopersicon esculentum	(Solanum lycopersicum)			
ORGANISM			Lycopersicon esculentum				
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
			Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
			asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.				
REFERENCE			1 (bases 1 to 191)				
AUTHORS			van der Hoeven,R.S., Bezzerides,J.l., Matern,A.L., Holt,I.E.,				
			Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,				
			Ronning,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and				
			Tanksley,S.D.				
			Generation of ESTs from tomato flower tissue				
TITLE							

Query Match 100.0%; Score 23; DB 1; Length 193;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 80 GGATAACCGTGGTAATTCTAGAG 58

RESULT 5  
AU009944  
LOCUS AU009944 200 bp mRNA linear EST 31-JUL-1998  
DEFINITION AU009944 Schizosaccharomyces pombe late log phase cDNA  
Schizosaccharomyces pombe cDNA clone spc00704, mRNA sequence.

ACCESSION AU009944 GI:3346624  
VERSION AU009944  
KEYWORDS EST.  
SOURCE Schizosaccharomyces pombe (fission yeast)  
ORGANISM Schizosaccharomyces pombe  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomycetes.

REFERENCE 1 (bases 1 to 200)  
AUTHORS Morimyo,M. and Mita,K.  
TITLE Identification of expressed sequence tags of Schizosaccharomyces

JOURNAL pombe  
COMMENT Unpublished (1998)  
Contact: Mitsuoki Morimyo  
Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: morimyo@nirs.go.jp.

FEATURES  
source  
1. .200  
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Schizosaccharomyces pombe was prepared by cloning cDNA  
into the SmaI site of M13mp19 DNA and the direction of DNA  
sequences was not always from 5' to 3'. The cDNA data of  
Schizosaccharomyces pombe are available for searching on  
the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 200;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 121 GGATAACCGTGGTAATTCTAGAG 143

RESULT 6  
AU010607  
LOCUS AU010607 208 bp mRNA linear EST 31-JUL-1998  
DEFINITION AU010607 Schizosaccharomyces pombe late log phase cDNA  
Schizosaccharomyces pombe cDNA clone spc10128, mRNA sequence.

ACCESSION AU010607 GI:3347287  
VERSION AU010607  
KEYWORDS EST.  
SOURCE Schizosaccharomyces pombe (fission yeast)  
ORGANISM Schizosaccharomyces pombe  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomycetes.

REFERENCE 1 (bases 1 to 208)

AUTHORS  
TITLE

JOURNAL  
COMMENT

FEATURES  
source

Morimyo,M. and Mita,K.  
Identification of expressed sequence tags of Schizosaccharomyces  
pombe  
Unpublished (1998)  
Contact: Mitsuoki Morimyo  
Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: morimyo@nirs.go.jp.

Location/Qualifiers

1. .208  
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Schizosaccharomyces pombe was prepared by cloning cDNA  
into the SmaI site of M13mp19 DNA and the direction of DNA  
sequences was not always from 5' to 3'. The cDNA data of  
Schizosaccharomyces pombe are available for searching on  
the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 208;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 129 GGATAACCGTGGTAATTCTAGAG 151

RESULT 7

AL749833

LOCUS

DEFINITION AL749833 AS Pinus pinaster cDNA clone AS01F05 similar to 18S, mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Pinus pinaster  
Pinus pinaster  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
1 (bases 1 to 216)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Identification of water-deficit responsive genes in Maritime pine  
(Pinus pinaster Ait.) using an EST approach  
Unpublished (2002)  
Contact: Frigerio JM  
Genetique et Amelioration 69  
INRA  
route d'Arcachon 33612 Cestas.CEDEX France  
Email: Frigerio@pierroton.inra.fr  
Seq primer: T3.

FEATURES

source

1. .216  
/organism="Pinus pinaster"  
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/clone="AS01F05"  
/tissue\_type="shoot"  
/dev\_stage="6 weeks old seedling"  
/lab\_host="SOLR"  
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/note="Vector: Uni-ZAP XR; ecotype: Landes; The library  
was made from the aerial part (above the collar) of 6  
weeks old seedlings grown in hydroponic conditions. A  
three weeks drought stress treatment was applied by  
lowering the osmotic potential of the nutrient solution to



-0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 216;  
Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
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Db 117 GGATAACCGTGGTAATTCTAGAG 139

RESULT 8

AW791051 222 bp mRNA linear EST 01-MAY-2001  
LOCUS D00369-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei  
DEFINITION cDNA clone D00369 similar to hypothetical protein 2, mRNA sequence.  
ACCESSION AW791051  
VERSION AW791051.1 GI:13902648  
KEYWORDS EST.  
SOURCE Blumeria graminis f. sp. hordei  
ORGANISM Blumeria graminis f. sp. hordei

REFERENCE

AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
Erysiphales; Erysiphaceae; Blumeria.  
1 (bases 1 to 222)  
Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rouster,J.A. and Oliver,R.P.

TITLE Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis

JOURNAL

COMMENT Unpublished (2000)  
Contact: Rasmussen,S.W.  
Department of Yeast Genetics  
Carlsberg Laboratory  
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark  
Tel: 45 3327 5230  
Fax: 45 3327 4766  
Email: swr@crc.dk  
High quality sequence stop: 222  
POLYA=No.

FEATURES

source Location/Qualifiers  
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/clone="D00369"  
/cell\_type="conidia"  
/lab\_host="Hordeum vulgare"  
/clone\_lib="Lambda Zap, Stratagene"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
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Db 173 GGATAACCGTGGTAATTCTAGAG 195

RESULT 9

CF945579 230 bp mRNA linear EST 19-NOV-2003  
LOCUS TrEST-A2815 TrEST-A Hypocrea jecorina cDNA clone Tr-A2815 5', mRNA  
DEFINITION sequence.  
ACCESSION CF945579  
VERSION CF945579.1 GI:38446099  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina

REFERENCE

AUTHORS

TITLE

JOURNAL  
PUBMED  
COMMENT

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 230)

Chambergo,F.S., Bonaccorsi,E.D., Ferreira,A.J.S., Ramos,A.S.P.,  
Ferreira,J.R.Jr., Abrahao-Neto,J., Farah,J.P.S. and El-Dorrry,H.  
Elucidation of the metabolic fate of glucose in the filamentous  
fungus Trichoderma reesei using expressed sequence tag (EST)  
analysis and cDNA microarrays  
J. Biol. Chem. 277 (16), 13983-13988 (2002)  
11825887

Contact: El-Dorrry, Hamza  
Department of Biochemistry  
Institute of Chemistry. University of Sao Paulo  
Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,  
BRASIL

Tel: (55) 11-38183848  
Fax: (55) 11-38183848  
Email: dorrry@iq.usp.br

PCR Primers

FORWARD: Universal M13 forward primer  
BACKWARD: Universal M13 reverse primer  
Plate: 30 row: C column: 7  
Seq primer: M13 reverse primer  
High quality sequence stop: 229  
POLYA=No.

FEATURES

source

Location/Qualifiers  
1..230  
/organism="Hypocrea jecorina"  
/mol\_type="mRNA"  
/strain="QM9414 (ATCC26921)"  
/db\_xref="taxon:51453"  
/clone="Tr-A2815"  
/sex="Asexual"  
/tissue\_type="Mycelia"  
/dev\_stage="18 hr Glycerol-grown culture"  
/lab\_host="E. coli SOLR cells (kanamycin resistant)"  
/clone\_lib="TrEST-A"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:  
XhoI; anamorph=Trichoderma reesei; Cloned  
unidirectionally, 5' end of the cDNA cloned into EcoRI  
site of pBluescript. Primer: Oligo (dT). Average insert  
size: 1,2 kb; Uni-ZAP XR Vector system -5' adaptor  
sequence: 5'GAATTCGGCAGG3' -3' adaptor sequence:  
5'CTCGAGTTTTTTTTTTTTTTT3' "

ORIGIN

Query Match 100.0%; Score 23; DB 7; Length 230;  
Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 132 GGATAACCGTGGTAATTCTAGAG 154

RESULT 10

CF945596 233 bp mRNA linear EST 19-NOV-2003  
LOCUS TrEST-A2885 TrEST-A Hypocrea jecorina cDNA clone Tr-A2885 5', mRNA  
DEFINITION sequence.  
ACCESSION CF945596  
VERSION CF945596.1 GI:38446116  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 233)

Chambergo,F.S., Bonaccorsi,E.D., Ferreira,A.J.S., Ramos,A.S.P.,  
Ferreira,J.R.Jr., Abrahao-Neto,J., Farah,J.P.S. and El-Dorrry,H.  
Elucidation of the metabolic fate of glucose in the filamentous  
fungus Trichoderma reesei using expressed sequence tag (EST)  
analysis and cDNA microarrays



JOURNAL  
PUBMED  
COMMENT

J. Biol. Chem. 277 (16), 13983-13988 (2002)  
11825887  
Contact: El-Dorry, Hamza  
Department of Biochemistry  
Institute of Chemistry. University of Sao Paulo  
Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,  
BRASIL  
Tel: (55) 11-38183848  
Fax: (55) 11-38183848  
Email: dorry@iq.usp.br  
PCR Primers  
FORWARD: Universal M13 forward primer  
BACKWARD: Universal M13 reverse primer  
Plate: 31 row: A column: 5  
Seq primer: M13 reverse primer  
High quality sequence stop: 232  
POLYA=No.

FEATURES  
source

Location/Qualifiers  
1. .233  
/organism="Hypocrea jecorina"  
/mol\_type="mRNA"  
/strain="QM9414 (ATCC26921)"  
/db\_xref="taxon:51453"  
/clone="Tr-A2885"  
/sex="Asexual"  
/tissue\_type="Mycelia"  
/dev\_stage="18 hr Glycerol-grown culture"  
/lab\_host="E. coli SOLR cells (kanamycin resistant)"  
/clone\_lib="TrEST-A"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site\_2:  
XhoI; anamorph=Trichoderma reesei; Cloned  
unidirectionally, 5' end of the cDNA cloned into EcoRI  
site of pBluescript. Primer: Oligo (dT). Average insert  
size: 1,2 kb; Uni-ZAP XR Vector system -5' adaptor  
sequence: 5'GAATTCGGCACGAG3' -3' adaptor sequence:  
5'CTCGAGTTTTTTTTTTTTTTT3'"

ORIGIN

Query Match 100.0%; Score 23; DB 7; Length 233;  
Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23  
|||||  
Db 125 GGATAACCGTGGTAATCTAGAG 147

ORIGIN

Query Match 100.0%; Score 23; DB 7; Length 233;  
Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23  
|||||  
Db 125 GGATAACCGTGGTAATCTAGAG 147

RESULT 11  
CF945185  
LOCUS

DEFINITION

CF945185  
CF945185.1 GI:38445705  
EST.  
Hypocrea jecorina (anamorph: Trichoderma reesei)  
Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 236)  
Chamberg, F.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P.,  
Ferreira, J.R.Jr., Abrahao-Neto, J., Farah, J.P.S. and El-Dorry, H.  
Elucidation of the metabolic fate of glucose in the filamentous  
fungus Trichoderma reesei using expressed sequence tag (EST)  
analysis and cDNA microarrays  
J. Biol. Chem. 277 (16), 13983-13988 (2002)  
11825887  
COMMENT

Contact: El-Dorry, Hamza  
Department of Biochemistry  
Institute of Chemistry. University of Sao Paulo  
Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,  
BRASIL  
Tel: (55) 11-38183848

JOURNAL  
PUBMED  
COMMENT

J. Biol. Chem. 277 (16), 13983-13988 (2002)  
11825887  
Contact: El-Dorry, Hamza  
Department of Biochemistry  
Institute of Chemistry. University of Sao Paulo  
Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,  
BRASIL  
Tel: (55) 11-38183848

Fax: (55) 11-38183848  
Email: dorry@iq.usp.br  
PCR Primers  
FORWARD: Universal M13 forward primer  
BACKWARD: Universal M13 reverse primer  
Plate: 30 row: G column: 7  
Seq primer: M13 reverse primer  
High quality sequence stop: 230  
POLYA=No.

FEATURES  
source

Location/Qualifiers  
1. .236  
/organism="Hypocrea jecorina"  
/mol\_type="mRNA"  
/strain="QM9414 (ATCC26921)"  
/db\_xref="taxon:51453"  
/clone="Tr-A2863"  
/sex="Asexual"  
/tissue\_type="Mycelia"  
/dev\_stage="18 hr Glycerol-grown culture"  
/lab\_host="E. coli SOLR cells (kanamycin resistant)"  
/clone\_lib="TrEST-A"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site\_2:  
XhoI; anamorph=Trichoderma reesei; Cloned  
unidirectionally, 5' end of the cDNA cloned into EcoRI  
site of pBluescript. Primer: Oligo (dT). Average insert  
size: 1,2 kb; Uni-ZAP XR Vector system -5' adaptor  
sequence: 5'GAATTCGGCACGAG3' -3' adaptor sequence:  
5'CTCGAGTTTTTTTTTTTTTTT3'"

ORIGIN

Query Match 100.0%; Score 23; DB 7; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23  
|||||  
Db 125 GGATAACCGTGGTAATCTAGAG 147

RESULT 12  
AA532319  
LOCUS

DEFINITION

AA532319  
AA532319.1 GI:2276511  
EST.  
Cryptosporidium parvum  
Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.  
1 (bases 1 to 254)  
Strong, W.B. and Nelson, R.G.  
Preliminary profile of the Cryptosporidium parvum genome: an  
expressed sequence tag and genome survey sequence analysis  
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)  
10717299  
COMMENT

Contact: Nelson, R. G.  
Depts. of Medicine & Pharmaceutical Chemistry  
San Francisco General Hospital-University of California, San  
Francisco  
Box 0811, San Francisco, CA 94143-0811, USA  
Tel: 415 206 8846  
Fax: 415 206 3353  
Email: malaria@itsa.ucsf.edu  
Submitted sequence has been edited to remove vector sequences 5' to  
the insert, to correct miscalled bases and assign uncalled (N)  
bases throughout the sequence, and to terminate when base-calling  
became ambiguous.  
Seq primer: M13 reverse  
High quality sequence stop: 254.  
Location/Qualifiers  
1. .254

/organism="Cryptosporidium parvum"  
/mol\_type="mRNA"  
/strain="IOWA"  
/db\_xref="taxon:5807"  
/dev\_stage="sporozoite"  
/lab\_host="E. coli XL1 Blue MRF' Kan"  
/clone\_lib="unizAPCPIOWAsporoLib3"  
/note="Vector: UNIZAP XR; Site 1: EcoR I; Site 2: Xho I;  
The C. parvum cDNA library was prepared by Drs. Norman J.  
Pieniazek, Michael J. Arrowood, Susan B. Slemenda, and Jan  
R. Mead at the Centers for Disease Control and Prevention  
(Atlanta, Georgia). Poly A+ RNA was separated from total  
C. parvum RNA using the Poly(A) Quik mRNA Isolation Kit  
from Stratagene. Directional cDNA was synthesized by  
first-strand priming with a Xho I-oligo d(T)  
linker-primer, second-stranding with RNase H and DNA  
polymerase I, ligation of EcoR I linkers, and digestion  
with Xho I, all using the Stratagene ZAP-cDNA synthesis  
kit. The cDNA was cloned into the EcoR I and Xho I sites  
of lambda Uni-ZAP XR vector; the unamplified library was  
>95% recombinant and contained 3.8 X 10(6) independent  
clones. PCR analysis of 20 random clones indicated that  
the average insert size was ca. 1.1 kb."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 114 GGATAACCGTGGTAATTCTAGAG 136

RESULT 13

CD029939  
LOCUS CD029939 256 bp mRNA linear EST 07-MAY-2003  
DEFINITION mgmk014xB02f.b pmk1 in pBluescriptII sk(-) plasmid Magnaporthe  
grisea cDNA clone mgmk014xB02 5', mRNA sequence.  
ACCESSION CD029939  
VERSION CD029939.1 GI:30411775  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
AUTHORS 1 (bases 1 to 256)  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhattearai,K. and Dean,R.A.  
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea

JOURNAL Unpublished (2002)  
COMMENT Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person;Best nr hit (April. 22, 2003) ref|XP\_284680.1| similar to  
hypothetical protein 2 (rRNA externa. . . 31 4.0  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgmk014 row: B column: 02  
Seq primer: T3.

FEATURES  
source Location/Qualifiers  
1. .256  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="NN95"  
/db\_xref="taxon:148305"

/clone="mgmk014xB02"  
/sex="Mat1-1 hermaphrodite"  
/cell\_type="germinated conidia"  
/clone\_lib="pmk1 in pBluescriptII sk(-) plasmid"  
/note="Vector: pBluescriptSK; Site 1: EcoRI; Site 2: XhoI;  
Conidia germinated in hydrophobic surface membrane in 27C  
for 12 hours. NN95 is a hygromycin phosphotransferase gene  
replacement of the PMK1 MAP kinase gene in the Guy11  
strain background (Xu and Hamer. 1996. Genes & Dev.  
10:2696). Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredPhrap version 991019 and trimmed  
according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 100.0%; Score 23; DB 6; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 109 GGATAACCGTGGTAATTCTAGAG 131

RESULT 14

AI398053  
LOCUS AI398053 269 bp mRNA linear EST 08-FEB-1999  
DEFINITION NCSC2C47 Subtracted Conidial Neurospora crassa cDNA clone SC2C4  
3', mRNA sequence.  
ACCESSION AI398053  
VERSION AI398053.1 GI:4241138  
KEYWORDS EST.  
SOURCE Neurospora crassa  
ORGANISM Neurospora crassa

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
AUTHORS 1 (bases 1 to 269)  
Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,  
Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,  
Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K.,  
Miller,R., Ortega,J., Pavlova,I., Perea,J., Todisco,S.,  
Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S.  
and Natvig,D.O.  
TITLE Expressed sequences from conidial, mycelial, and sexual stages of  
Neurospora crassa  
JOURNAL Fungal Genet. Biol. 21, 348-363 (1997)  
PUBMED 9290248  
COMMENT Contact: Natvig,D.O./Nelson,M.A.  
Department of Biology  
University of New Mexico  
Castetter Hall, Albuquerque, NM 87131, USA  
Tel: 505 277 3411  
Fax: 505 277 0304  
Email: ngp@biology.unm.edu.  
Location/Qualifiers  
1. .269  
/organism="Neurospora crassa"  
/mol\_type="mRNA"  
/strain="74-OR23-IV A (FGSC 2489)"  
/db\_xref="taxon:5141"  
/clone="SC2C4"  
/sex="Mating Type A"  
/tissue\_type="Conidia"  
/dev\_stage="Germinating conidia"  
/lab\_host="E. coli"  
/clone\_lib="Subtracted Conidial"  
/note="Vector: pBluescript SK (-); Site 1: EcoRI; Site 2:  
XhoI; mRNA isolated from germinating conidia, grown in 1x  
Vogel's, 2% sucrose for 4.5 hours. cDNA directionally  
cloned into pBluescript SK(-) using the Uni-ZAP XR vector  
system (Stratagene, La Jolla, CA). Previously identified

highly expressed clones were subtracted from this library."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 269;  
Best Local Similarity 100.0%; Pred. No. 0.66;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGATAACCGTGGTAATCTAGAG 23  
|||||  
Db 220 GGATAACCGTGGTAATCTAGAG 242

RESULT 15  
BU638475 278 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcw009xE23f.b RCW Lambda Zap Express Library Magnaporthe grisea  
DEFINITION cDNA clone mgcw009xE23 5', mRNA sequence.  
ACCESSION BU638475  
VERSION BU638475.1 GI:23350801  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
REFERENCE 1 (bases 1 to 278)  
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.  
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea  
JOURNAL Unpublished (2002)  
COMMENT Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) gb|EAA21331.1| hypothetical protein [Plasmodium yoelii yoelii] 35 0.21  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcw009 row: E column: 23  
Seq primer: T3.

FEATURES

source Location/Qualifiers  
1..278  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="CP987"  
/db\_xref="taxon:148305"  
/clone="mgcw009xE23"  
/sex="Mat1-1 hermaphrodite"  
/tissue\_type="Mycelium"  
/dev\_stage="Day 5 post-inoculation"  
/clone\_lib="RCW Lambda Zap Express Library"  
/note="Vector: pBluescript excised from Lambda Zap Express; Site 1: EcoRI; Site 2: XhoI; Day 5 post-inoculation mRNAs prepared from Magnaporthe grisea grown at 23C in the dark with constant gyratory shaking 100 rpm in Vogel's minimal medium containing 0.5% isolated rice cell walls as the sole carbon source. Library provided by Sheng-Cheng Wu. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

ORIGIN

Query Match 100.0%; Score 23; DB 5; Length 278;

Best Local Similarity 100.0%; Pred. No. 0.66;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGATAACCGTGGTAATCTAGAG 23  
|||||  
Db 1 GGATAACCGTGGTAATCTAGAG 23  
  
Search completed: January 9, 2006, 21:16:55  
Job time : 2480 secs

**this Page Blank (uspio)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using -sw model

Run on: January 9, 2006, 18:17:01 ; Search time 102.5 Seconds  
(without alignments)  
398.867 Million cell updates/sec

Title: US-09-954-586-46  
Perfect score: 23  
Sequence: 1 ggataaccgtggtaattcttag 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq: \*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq: \*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	444	2	US-08-093-144-5
2	23	100.0	444	2	US-08-093-144-6
3	23	100.0	446	2	US-08-093-144-4
4	23	100.0	570	3	US-09-533-559-1021
5	23	100.0	617	3	US-09-533-559-3436
6	23	100.0	1750	3	US-08-949-770-1
7	23	100.0	1788	2	US-08-867-820A-1
8	23	100.0	2055	3	US-10-121-740-3
9	23	100.0	2089	3	US-10-121-740-1
10	23	100.0	2293	3	US-09-645-073-1
11	21.4	93.0	25	3	US-09-396-196G-761
12	21.4	93.0	40	2	US-07-720-587A-2
13	21.4	93.0	312	3	US-09-270-767-10466
14	21.4	93.0	1665	3	US-09-805-127-7
15	21.4	93.0	22118	3	US-09-815-981A-5
16	20	87.0	1747	2	US-08-327-516-1
17	20	87.0	1747	3	US-09-281-766-1
18	20	87.0	1747	3	US-09-612-858-1
19	20	87.0	1747	3	US-09-957-995A-1
20	19.8	86.1	568	3	US-09-533-559-4068
21	19.8	86.1	703	3	US-08-998-416-178
22	19.8	86.1	706	3	US-08-998-416-814
23	19.8	86.1	709	3	US-08-998-416-281
24	19.8	86.1	712	3	US-08-998-416-910

c	25	19.8	86.1	717	3	US-08-998-416-602	Sequence 602, Appl
	26	19.8	86.1	723	3	US-08-998-416-952	Sequence 952, Appl
	27	19.8	86.1	1608	2	US-08-899-371-2	Sequence 2, Appli
	28	19.8	86.1	1759	3	US-10-052-092-25	Sequence 25, Appl
c	29	19.8	86.1	1776	3	US-09-350-710B-1	Sequence 1, Appli
	30	18.4	80.0	1744	2	US-07-879-647A-25	Sequence 25, Appl
	31	18.4	80.0	1744	2	US-07-879-584A-25	Sequence 25, Appl
	32	18.4	80.0	1744	2	US-07-879-470A-25	Sequence 25, Appl
	33	18.4	80.0	1744	2	US-07-879-644A-25	Sequence 25, Appl
	34	18.4	80.0	1744	2	US-07-879-640A-25	Sequence 25, Appl
	35	18.4	80.0	1744	2	US-07-879-594A-25	Sequence 25, Appl
	36	18.4	80.0	1744	2	US-07-879-469A-25	Sequence 25, Appl
	37	18.4	80.0	1747	2	US-07-879-647A-29	Sequence 29, Appl
	38	18.4	80.0	1747	2	US-07-879-584A-29	Sequence 29, Appl
	39	18.4	80.0	1747	2	US-07-879-470A-29	Sequence 29, Appl
	40	18.4	80.0	1747	2	US-07-879-644A-29	Sequence 29, Appl
	41	18.4	80.0	1747	2	US-07-879-640A-29	Sequence 29, Appl
	42	18.4	80.0	1747	2	US-07-879-594A-29	Sequence 29, Appl
	43	18.4	80.0	1747	2	US-07-879-469A-29	Sequence 29, Appl
	44	18.4	80.0	1747	3	US-09-015-259-1	Sequence 1, Appli
	45	18.4	80.0	1747	3	US-09-015-259-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-093-144-5  
; Sequence 5, Application US/08093144  
; Patent No. 5434048  
; GENERAL INFORMATION:  
; APPLICANT: SIMON, LUC  
; APPLICANT: LALONDE, MAURICE  
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF  
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: Eleventh Floor, 1615 L. Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/093,144  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,192  
; FILING DATE: 15-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hymo, Lawrence A.  
; REGISTRATION NUMBER: 19,057  
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 444 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-093-144-5

Query Match 100.0%; Score 23; DB 2; Length 444;  
Best Local Similarity 100.0%; Pred. No. 0.094;

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCTAGAG 23
    |||||
Db 33 GGATAACCGTGGTAATTCTAGAG 55

RESULT 2
US-08-093-144-6
; Sequence 6, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-6

Query Match 100.0%; Score 23; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCTAGAG 23
    |||||
Db 33 GGATAACCGTGGTAATTCTAGAG 55

RESULT 3
US-08-093-144-4
; Sequence 4, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
```

```
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-4

Query Match 100.0%; Score 23; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCTAGAG 23
    |||||
Db 32 GGATAACCGTGGTAATTCTAGAG 54

RESULT 4
US-09-533-559-1021/c
; Sequence 1021, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1021
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(570)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1021

Query Match 100.0%; Score 23; DB 3; Length 570;
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Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23
Db 422 GGATAACCGTGGTAATTCTAGAG 400

RESULT 5
US-09-533-559-3436
; Sequence 3436, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; EARLIER FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3436
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(617)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-3436

Query Match 100.0%; Score 23; DB 3; Length 617;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23
Db 125 GGATAACCGTGGTAATTCTAGAG 147

RESULT 6
US-08-949-770-1
; Sequence 1, Application US/08949770
; Patent No. 6063604
; GENERAL INFORMATION:
; APPLICANT: Wick, James F.
; APPLICANT: Mueller, Reinhold
; APPLICANT: Blassak, Michele
; APPLICANT: Wilkosz, Richard K.
; TITLE OF INVENTION: Target Nucleic Acid Sequence Amplification
; Patent No. 6063604
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,770
```

```
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/617,045
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 28003/33045
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "18s rRNA gene of Cryptosporidium"
OTHER INFORMATION: parvum"
US-08-949-770-1

Query Match 100.0%; Score 23; DB 3; Length 1750;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23
Db 141 GGATAACCGTGGTAATTCTAGAG 163

RESULT 7
US-08-867-820A-1
; Sequence 1, Application US/08867820A
; Patent No. 5891685
; GENERAL INFORMATION:
; APPLICANT: YAMAGISHI Masahiro
; APPLICANT: TAKAI Yukie
; APPLICANT: MIKAWA Takashi
; APPLICANT: HARA Mari
; APPLICANT: UEDA Makoto
; APPLICANT: OHARA Akiko
; TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S) - -HALOGENATED- -HYDROXYBUTY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,820A
; FILING DATE: June 3, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 1416/OP574US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs
```



```

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
; STRAIN: MUCL29800
US-08-867-820A-1

Query Match      100.0%; Score 23; DB 2; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAGAG 23
      |||||||
Db      141 GGATAACCGTGGTAATTCTAGAG 163

RESULT 8
US-10-121-740-3
; Sequence 3, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-121-740-3

Query Match      100.0%; Score 23; DB 3; Length 2055;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAGAG 23
      |||||||
Db      124 GGATAACCGTGGTAATTCTAGAG 146

RESULT 9
US-10-121-740-1
; Sequence 1, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2089
; TYPE: DNA
; ORGANISM: Muscodor albus
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```

US-10-121-740-1

Query Match      100.0%; Score 23; DB 3; Length 2089;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAGAG 23
      |||||||
Db      137 GGATAACCGTGGTAATTCTAGAG 159

RESULT 10
US-09-645-073-1
; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titer of Gibberellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
US-09-645-073-1

Query Match      100.0%; Score 23; DB 3; Length 2293;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAGAG 23
      |||||||
Db      117 GGATAACCGTGGTAATTCTAGAG 139

RESULT 11
US-09-396-196G-761
; Sequence 761, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-761

Query Match      93.0%; Score 21.4; DB 3; Length 25;
Best Local Similarity 95.7%; Pred. No. 0.45;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAGAG 23
      |||||||
Db      1 GGATAACTGTGGTAATTCTAGAG 23
```

RESULT 12  
US-07-720-587A-2/c  
; Sequence 2, Application US/07720587A  
; Patent No. 5352579  
; GENERAL INFORMATION:  
; APPLICANT: Curt L. Milliman  
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES  
; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: Wordperfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/720,587A  
; FILING DATE: 19910628  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 193/121  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-720-587A-2

Query Match 93.0%; Score 21.4; DB 2; Length 40;  
Best Local Similarity 95.7%; Pred. No. 0.47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
Db 29 GGATAACCGTGGTAATTCTAGAG 7

RESULT 13  
US-09-270-767-10466  
; Sequence 10466, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10466  
; LENGTH: 312  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-10466

Query Match 93.0%; Score 21.4; DB 3; Length 312;  
Best Local Similarity 95.7%; Pred. No. 0.55;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
Db 142 GGATAACTGTGGTAATTCTAGAG 164

RESULT 14  
US-09-805-127-7  
; Sequence 7, Application US/09805127  
; Patent No. 6653119  
; GENERAL INFORMATION:  
; APPLICANT: BIO MEDIATION TECHNOLOGIE, INC.  
; TITLE OF INVENTION: WHITE ROT FUNGI AND METHOD FOR DECOMPOSING DIOXINS USING THEM  
; FILE REFERENCE: WKO-101PCT  
; CURRENT APPLICATION NUMBER: US/09/805,127  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: JP 1998-260707  
; PRIOR FILING DATE: 1998-09-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 1665  
; TYPE: DNA  
; ORGANISM: White rod fungus MZ-340  
US-09-805-127-7

Query Match 93.0%; Score 21.4; DB 3; Length 1665;  
Best Local Similarity 95.7%; Pred. No. 0.62;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
Db 88 GGATAACTGTGGTAATTCTAGAG 110

RESULT 15  
US-09-815-981A-5  
; Sequence 5, Application US/09815981A  
; Patent No. 6936469  
; GENERAL INFORMATION:  
; APPLICANT: de Jong, Gary  
; APPLICANT: Vandebyl, Sandra  
; TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID  
; TITLE OF INVENTION: MOLECULES INTO CELLS AND ASSESSMENT THEREOF  
; FILE REFERENCE: 24601-416B  
; CURRENT APPLICATION NUMBER: US/09/815,981A  
; CURRENT FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 22118  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-815-981A-5

Query Match 93.0%; Score 21.4; DB 3; Length 22118;  
Best Local Similarity 95.7%; Pred. No. 0.76;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
Db 9787 GGATAACTGTGGTAATTCTAGAG 9809

Search completed: January 9, 2006, 21:20:28  
Job time : 105.5 secs

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; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-52

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.18;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23
| | | | | | | | | | | | | | | | | | |
Db 1 GGAUAACCGUGGUAUUCUAGAG 23

RESULT 3
US-09-954-695-58/c
; Sequence 58, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-58

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23
| | | | | | | | | | | | | | | | | | |
Db 23 GGATAACCGTGGTAATTCTAGAG 1

RESULT 4
US-09-954-695-64/c
; Sequence 64, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 64
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-64

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23
| | | | | | | | | | | | | | | | | | |
Db 23 GGATAACCGTGGTAATTCTAGAG 1

RESULT 5
US-09-954-586-46
; Sequence 46, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-46

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23
| | | | | | | | | | | | | | | | | | |
Db 1 GGATAACCGTGGTAATTCTAGAG 23

RESULT 6
US-09-954-586-52
; Sequence 52, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Synthetic Construct
US-09-954-586-52

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.18;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAG 23
      |||:|||||:|:|:|:|:|
Db      1 GGAUAACCGUGGUAUUCUAG 23

RESULT 7
US-09-954-586-58/c
; Sequence 58, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-58

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAG 23
      |||:|||||:|:|:|:|:|
Db      23 GGATAACCGTGGTAATTCTAG 1

RESULT 8
US-09-954-586-64/c
; Sequence 64, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-64

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAG 23
      |||:|||||:|:~|:~|:~|:~|
Db      23 GGATAACCGTGGTAATTCTAG 1

RESULT 9
US-09-954-695-29
; Sequence 29, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-29

Query Match      100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAG 23
      |||:|||||:~|:~|:~|:~|
Db      1 GGATAACCGTGGTAATTCTAG 23

RESULT 10
US-09-954-695-33
; Sequence 33, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-33

Query Match      100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 73.9%; Pred. No. 0.19;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATAACCGTGGTAATTCTAG 23
      |||:|||||:~|:~|:~|:~|
Db      1 GGAUAACCGUGGUAUUCUAG 23
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RESULT 11  
US-09-954-695-37/c  
; Sequence 37, Application US/09954695  
; Patent No. US20020055116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-02.UT  
; CURRENT APPLICATION NUMBER: US/09/954,695  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-37

Query Match 100.0%; Score 23; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 32 GGATAACCGTGGTAATTCTAGAG 10

RESULT 12  
US-09-954-695-41/c  
; Sequence 41, Application US/09954695  
; Patent No. US20020055116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-02.UT  
; CURRENT APPLICATION NUMBER: US/09/954,695  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 32  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-41

Query Match 100.0%; Score 23; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 32 GGATAACCGTGGTAATTCTAGAG 10

RESULT 13  
US-09-954-586-29  
; Sequence 29, Application US/09954586

; Patent No. US20020146717A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-03.UT  
; CURRENT APPLICATION NUMBER: US/09/954,586  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-586-29

Query Match 100.0%; Score 23; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||||  
Db 1 GGATAACCGTGGTAATTCTAGAG 23

RESULT 14  
US-09-954-586-33  
; Sequence 33, Application US/09954586  
; Patent No. US20020146717A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-03.UT  
; CURRENT APPLICATION NUMBER: US/09/954,586  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 32  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-586-33

Query Match 100.0%; Score 23; DB 3; Length 32;  
Best Local Similarity 73.9%; Pred. No. 0.19;  
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
|||:|||||:|:|:|:|  
Db 1 GGAUAACCGUGGUAUUCUAGAG 23

RESULT 15  
US-09-954-586-37/c  
; Sequence 37, Application US/09954586  
; Patent No. US20020146717A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.



; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-37

Query Match 100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCTAGAG 23
Db 32 GGATAACCGTGGTAATTCTAGAG 10

Search completed: January 10, 2006, 00:04:32
Job time : 518 secs

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November 2005

Published\_Applications\_Nucleic Acid and Published\_Applications\_Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rppbm** (Published\_Applications\_NA\_Main) and **.rnpbm** (Published\_Applications\_NA\_New). Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 21:17:07 ; Search time 215 Seconds  
(without alignments)  
77.993 Million cell updates/sec

Title: US-09-954-586-46  
Perfect score: 23  
Sequence: 1 ggataaccgtggttaattctagag 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:\*  
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2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
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9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3:\*  
10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	100.0	1732	6	US-10-519-379-1
2	21.4	93.0	1874	7	US-11-136-527-4032
3	21.4	93.0	1920	7	US-11-136-527-174864
4	21.4	93.0	1920	7	US-11-136-527-174865
5	21.4	93.0	1920	7	US-11-136-527-174866
6	21.4	93.0	1969	6	US-10-775-169-210
7	21.4	93.0	1969	6	US-10-947-249-33
8	21.4	93.0	59590	7	US-11-117-187-187
9	16.6	72.2	1391	6	US-10-750-185-31917
10	16.6	72.2	1391	6	US-10-750-623-31917
11	16.6	72.2	1542	6	US-10-873-528-205
12	16.6	72.2	1542	6	US-10-873-528-245
13	16.4	71.3	3688	6	US-10-750-185-30025
14	16.4	71.3	3688	6	US-10-750-623-30025
15	15.8	68.7	19	8	US-11-101-244-1440038
16	15.8	68.7	19	9	US-11-083-784-1440038
17	15.8	68.7	235033	7	US-11-157-389-1
18	15.8	68.7	237326	7	US-11-157-389-2
19	15.6	67.8	201	6	US-10-995-561-24091
20	15.6	67.8	600	6	US-10-750-185-1120
21	15.6	67.8	600	6	US-10-750-623-1120
22	15.6	67.8	159138	6	US-10-995-561-13230
23	15.4	67.0	1983	6	US-10-750-185-50579

C	24	15.4	67.0	1983	6	US-10-750-623-50579	Sequence 50579, A
	25	15.2	66.1	913	6	US-10-750-185-38513	Sequence 38513, A
	26	15.2	66.1	913	6	US-10-750-623-38513	Sequence 38513, A
	27	15.2	66.1	1128	6	US-10-750-185-41157	Sequence 41157, A
	28	15.2	66.1	1128	6	US-10-750-623-41157	Sequence 41157, A
C	29	15.2	66.1	1144	7	US-11-136-527-4058	Sequence 4058, Ap
C	30	15.2	66.1	1144	7	US-11-136-527-8154	Sequence 8154, Ap
	31	15.2	66.1	1525	6	US-10-750-185-40363	Sequence 40363, A
	32	15.2	66.1	1525	6	US-10-750-623-40363	Sequence 40363, A
C	33	15.2	66.1	2444	7	US-11-136-527-3546	Sequence 3546, Ap
C	34	15.2	66.1	96583	7	US-11-117-187-203	Sequence 203, App
C	35	15.2	66.1	105550	6	US-10-995-561-13235	Sequence 13235, A
	36	15	65.2	294	6	US-10-467-657-5153	Sequence 5153, Ap
	37	15	65.2	967	6	US-10-750-185-27830	Sequence 27830, A
	38	15	65.2	967	6	US-10-750-623-27830	Sequence 27830, A
C	39	15	65.2	1627	6	US-10-750-185-28345	Sequence 28345, A
C	40	15	65.2	1627	6	US-10-750-623-28345	Sequence 28345, A
C	41	15	65.2	1771	6	US-10-750-185-61743	Sequence 61743, A
C	42	15	65.2	1771	6	US-10-750-623-61743	Sequence 61743, A
	43	15	65.2	2699	7	US-11-064-246-6	Sequence 6, Appli
	44	15	65.2	2699	7	US-11-064-246-8	Sequence 8, Appli
C	45	15	65.2	129021	7	US-11-117-187-202	Sequence 202, App

ALIGNMENTS

RESULT 1  
US-10-519-379-1  
; Sequence 1, Application US/10519379  
; Publication No. US20050255126A1  
; GENERAL INFORMATION:  
; APPLICANT: ASahi DENKA Co., Ltd.  
; TITLE OF INVENTION: New microorganism and method for producing aglucan by the new  
; TITLE OF INVENTION: microorganism  
; FILE REFERENCE: A0301  
; CURRENT APPLICATION NUMBER: US/10/519,379  
; CURRENT FILING DATE: 2004-12-27  
; NUMBER OF SEQ ID NOS: 4  
; SEQ ID NO 1  
; LENGTH: 1732  
; TYPE: DNA  
; ORGANISM: Aureobasidium pullulans ADK-34  
US-10-519-379-1

Query Match 100.0%; Score 23; DB 6; Length 1732;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCCTAGAG 23  
Db 102 GGATAACCGTGGTAATTCCTAGAG 124

RESULT 2  
US-11-136-527-4032  
; Sequence 4032, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4032  
; LENGTH: 1874  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus

US-11-136-527-4032

Query Match 93.0%; Score 21.4; DB 7; Length 1874;  
Best Local Similarity 95.7%; Pred. No. 0.09;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
||||| ||||||| |||||||  
Db 145 GGATAACTGTGGTAATTCTAGAG 167

RESULT 3

US-11-136-527-174864

; Sequence 174864, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 174864  
; LENGTH: 1920  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-174864

Query Match 93.0%; Score 21.4; DB 7; Length 1920;  
Best Local Similarity 95.7%; Pred. No. 0.091;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
||||| ||||||| ||||||| |||||||  
Db 154 GGATAACTGTGGTAATTCTAGAG 176

RESULT 4

US-11-136-527-174865

; Sequence 174865, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 174865  
; LENGTH: 1920  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-174865

Query Match 93.0%; Score 21.4; DB 7; Length 1920;  
Best Local Similarity 95.7%; Pred. No. 0.091;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
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Db 154 GGATAACTGTGGTAATTCTAGAG 176

RESULT 5

US-11-136-527-174866

; Sequence 174866, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 174866  
; LENGTH: 1920  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-174866

Query Match 93.0%; Score 21.4; DB 7; Length 1920;  
Best Local Similarity 95.7%; Pred. No. 0.091;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
||||| ||||||| ||||||| |||||||  
Db 154 GGATAACTGTGGTAATTCTAGAG 176

RESULT 6

US-10-775-169-210

; Sequence 210, Application US/10775169  
; Publication No. US20050287532A9  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael  
; APPLICANT: Twine, Natalie  
; APPLICANT: Dörner, Andrew  
; APPLICANT: Trepicchio, William  
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
; FILE REFERENCE: AM101080 (031896-013000)  
; CURRENT APPLICATION NUMBER: US/10/775,169  
; CURRENT FILING DATE: 2004-02-11  
; NUMBER OF SEQ ID NOS: 5278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 210  
; LENGTH: 1969  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (57)..(61)  
; OTHER INFORMATION: Each "n" represents a nucleotide selected from a, t, g or c, or  
; OTHER INFORMATION: contains no nucleotide.  
US-10-775-169-210

Query Match 93.0%; Score 21.4; DB 6; Length 1969;  
Best Local Similarity 95.7%; Pred. No. 0.091;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
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Db 246 GGATAACTGTGGTAATTCTAGAG 268

RESULT 7

US-10-947-249-33

; Sequence 33, Application US/10947249  
; Publication No. US20050287541A1  
; GENERAL INFORMATION:  
; APPLICANT: Akira NAKAGAWARA  
; APPLICANT: Miki OHIRA  
; APPLICANT: Shin ISHII  
; APPLICANT: Takeshi GOTO



APPLICANT: HIROYUKI KUBO  
APPLICANT: TAKAHIRO HIRATA  
APPLICANT: YASUKO YOSHIDA  
APPLICANT: SAICHI YAMADA  
TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Meth  
TITLE OF INVENTION: Predicting the Prognosis of Neuroblastoma  
FILE REFERENCE: 117007  
CURRENT APPLICATION NUMBER: US/10/947,249  
CURRENT FILING DATE: 2004-09-23  
PRIOR APPLICATION NUMBER: US 60/505,614  
PRIOR APPLICATION NUMBER: 2003-09-25  
NUMBER OF SEQ ID NOS: 200  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 33  
LENGTH: 1969  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (57)..(61)  
OTHER INFORMATION: n is a, t, g or c  
US-10-947-249-33

Query Match 93.0%; Score 21.4; DB 6; Length 1969;  
Best Local Similarity 95.7%; Pred. No. 0.091;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23  
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Db 246 GGATAACTGTGGTAATTTCTAGAG 268

RESULT 8

US-11-117-187-187  
Sequence 187, Application US/11117187  
Publication No. US20050266560A1  
GENERAL INFORMATION:  
APPLICANT: PREUSS, DAPHNE  
APPLICANT: COPENHAVER, GREGORY  
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS  
FILE REFERENCE: ARCD:309US  
CURRENT APPLICATION NUMBER: US/11/117,187  
CURRENT FILING DATE: 2005-04-28  
PRIOR APPLICATION NUMBER: US/09/531,120  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/125,219  
PRIOR FILING DATE: 1999-03-18  
NUMBER OF SEQ ID NOS: 212  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 187  
LENGTH: 5950  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: modified base  
LOCATION: (2521)..(57768)  
OTHER INFORMATION: N = A, C G, or T/U  
US-11-117-187-187

Query Match 93.0%; Score 21.4; DB 7; Length 5950;  
Best Local Similarity 95.7%; Pred. No. 0.17;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23  
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Db 42882 GGATAACCGTAGTAATTTCTAGAG 42904

RESULT 9

US-10-750-185-31917/c  
Sequence 31917, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 31917  
LENGTH: 1391  
TYPE: DNA  
ORGANISM: Bovine 19866881168939  
US-10-750-185-31917

Query Match 72.2%; Score 16.6; DB 6; Length 1391;  
Best Local Similarity 82.6%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23  
|||||  
Db 880 GGATAACTGTGGTAATTTGAAAG 858

RESULT 10

US-10-750-623-31917/c  
Sequence 31917, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 31917  
LENGTH: 1391  
TYPE: DNA  
ORGANISM: Bovine 19866881168939  
US-10-750-623-31917

Query Match 72.2%; Score 16.6; DB 6; Length 1391;  
Best Local Similarity 82.6%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23  
|||||  
Db 880 GGATAACTGTGGTAATTTGAAAG 858

RESULT 11

US-10-873-528-205  
Sequence 205, Application US/10873528  
Publication No. US20050276814A1  
GENERAL INFORMATION:  
APPLICANT: Microbial Technics Limited  
APPLICANT: Gilbert, Christophe FG  
APPLICANT: Hansbro, Philip M

; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; CURRENT FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 205  
; LENGTH: 1542  
; TYPE: DNA  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-205

Query Match 72.2%; Score 16.6; DB 6; Length 1542;  
Best Local Similarity 82.6%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
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Db 336 GGATAAACGTTTAAATTCTAAAG 358

RESULT 12  
US-10-873-528-245  
; Sequence 245, Application US/10873528  
; Publication No. US20050276814A1  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; CURRENT FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 245  
; LENGTH: 1542  
; TYPE: DNA  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-245

Query Match 72.2%; Score 16.6; DB 6; Length 1542;  
Best Local Similarity 82.6%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCTAGAG 23  
||||| ||| ||||||| ||  
Db 336 GGATAAACGTTTAAATTCTAAAG 358

RESULT 13  
US-10-750-185-30025/c  
; Sequence 30025, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30025  
; LENGTH: 3688  
; TYPE: DNA  
; ORGANISM: Bovine 19866881048613  
US-10-750-185-30025

Query Match 71.3%; Score 16.4; DB 6; Length 3688;  
Best Local Similarity 94.4%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATAACCGTGGTAATTCTA 20  
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Db 2394 ATAACCATGGTAATTCTA 2377

RESULT 14  
US-10-750-623-30025/c  
; Sequence 30025, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30025  
; LENGTH: 3688  
; TYPE: DNA  
; ORGANISM: Bovine 19866881048613  
US-10-750-623-30025

Query Match 71.3%; Score 16.4; DB 6; Length 3688;  
Best Local Similarity 94.4%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATAACCGTGGTAATTCTA 20  
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Db 2394 ATAACCATGGTAATTCTA 2377

RESULT 15  
US-11-101-244-1440038/c  
; Sequence 1440038, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244

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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1440038
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1440038

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Query Match	68.7%	Score 15.8;	DB 8;	Length 19;
Best Local Similarity	89.5%	Pred. NO. 34;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

**Qy**            5 AACCGTGGTAATTCTAGAG 23  
               ||| ||||| ||||| ||  
**Db**            19 AACAGTGGTAATTCTATAG 1

Search completed: January 10, 2006, 00:11:52  
Job time : 217 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 18:14:32 ; Search time 2255 Seconds  
(without alignments)  
579.778 Million cell updates/sec

Title: US-09-954-586-59  
Perfect score: 23  
Sequence: 1 ccgtaaagttattatgagtcacc 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

ALIGNMENTS

RESULT 1	AX421401/c	AX421401	23 bp	DNA	linear	PAT 18-JUN-2002
LOCUS	Sequence 47 from Patent WO0222890.					
DEFINITION	AX421401					
ACCESSION	AX421401					
VERSION	AX421401.1	GI:21524796				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Cunningham,M.M., Stull,P.D. and Weisburg,W.G.					
TITLE	Compositions, methods and kits for determining the presence of cryptosporidium organisms in a test sample					
JOURNAL	Patent: WO 0222890-A 47 21-MAR-2002;					
FEATURES	Gen-Probe Incorporated (US)					
source	Location/Qualifiers					
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ORIGIN						
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Best Local Similarity	100.0%;	Pred. No. 17;				
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Db	23 CCGTAAAGTTATTATGAGTCACC 1					
RESULT 2	AX421407/c	AX421407	23 bp	RNA	linear	PAT 18-JUN-2002
LOCUS	Sequence 53 from Patent WO0222890.					
DEFINITION	AX421407					
ACCESSION	AX421407					
VERSION	AX421407.1	GI:21524802				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM						

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	23	100.0	23	6	AX421407	AX421407 Sequence
C 3	23	100.0	23	6	AX421413	AX421413 Sequence
C 4	23	100.0	23	6	AX421419	AX421419 Sequence
C 5	23	100.0	413	2	AY508962	AY508962 Cryptospo
C 6	23	100.0	415	2	AY508963	AY508963 Cryptospo
C 7	23	100.0	600	2	AF262332	AF262332 Cryptospo
C 8	23	100.0	646	2	DQ003721	DQ003721 Cryptospo
C 9	23	100.0	660	2	AF316630	AF316630 Cryptospo
C 10	23	100.0	665	2	AF316631	AF316631 Cryptospo
C 11	23	100.0	704	2	CP18RRNA1	AF162429 Cryptospo
C 12	23	100.0	712	2	DQ067569	DQ067569 Cryptospo
C 13	23	100.0	715	2	AF262326	AF262326 Cryptospo
C 14	23	100.0	744	2	AY268582	AY268582 Cryptospo
C 15	23	100.0	748	2	AY268583	AY268583 Cryptospo
C 16	23	100.0	755	2	AY504517	AY504517 Cryptospo
C 17	23	100.0	769	2	DQ067565	DQ067565 Cryptospo
C 18	23	100.0	770	2	AY741305	AY741305 Cryptospo

other sequences; artificial sequences.	
1	
Cunningham,M.M., Stull,P.D. and Weisburg,W.G.	
Compositions, methods and kits for determining the presence of	
cryptosporidium organisms in a test sample	
Patent: WO 0222890-A 53 21-MAR-2002;	
Gen-Probe Incorporated (US)	
Location/Qualifiers	
source	
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Best Local Similarity	100.0%; Pred. No. 17;
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCGTAAAGTTATTATGAGTCACC 23 
Db	23 CCGTAAAGTTATTATGAGTCACC 1 
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AX421413	
LOCUS	AX421413 23 bp DNA linear PAT 18-JUN-2002
DEFINITION	Sequence 59 from Patent WO0222890.
ACCESSION	AX421413
VERSION	AX421413.1 GI:21524808
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
other sequences; artificial sequences.	
1	
Cunningham,M.M., Stull,P.D. and Weisburg,W.G.	
Compositions, methods and kits for determining the presence of	
cryptosporidium organisms in a test sample	
Patent: WO 0222890-A 59 21-MAR-2002;	
Gen-Probe Incorporated (US)	
Location/Qualifiers	
source	
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ORIGIN	
Query Match	100.0%; Score 23; DB 6; Length 23;
Best Local Similarity	100.0%; Pred. No. 17;
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCGTAAAGTTATTATGAGTCACC 23 
Db	1 CCGTAAAGTTATTATGAGTCACC 23 
RESULT 4	
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LOCUS	AX421419 23 bp RNA linear PAT 18-JUN-2002
DEFINITION	Sequence 65 from Patent WO0222890.
ACCESSION	AX421419
VERSION	AX421419.1 GI:21524814
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
other sequences; artificial sequences.	
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Cunningham,M.M., Stull,P.D. and Weisburg,W.G.	
Compositions, methods and kits for determining the presence of	
cryptosporidium organisms in a test sample	
Patent: WO 0222890-A 65 21-MAR-2002;	
Gen-Probe Incorporated (US)	
Location/Qualifiers	
source	
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/mol_type="unassigned DNA"	
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ORIGIN	
Query Match	100.0%; Score 23; DB 6; Length 23;
Best Local Similarity	100.0%; Pred. No. 17;
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCGTAAAGTTATTATGAGTCACC 23 
Db	1 CCGTAAAGTTATTATGAGTCACC 23 
RESULT 5	
AY508962	
LOCUS	AY508962 413 bp DNA linear INV 25-FEB-2004
DEFINITION	Cryptosporidium parvum strain Fox3 18S ribosomal RNA gene, partial sequence.
ACCESSION	AY508962
VERSION	AY508962.1 GI:42716333
KEYWORDS	.
SOURCE	Cryptosporidium parvum
ORGANISM	Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;	
Cryptosporidiidae; Cryptosporidium.	
1 (bases 1 to 413)	
Nagano,Y., Finn,M.B., Lowery,C.J., Murphy,T., McCorry,K.A.,	
Crothers,E., Watabe,M., Rao,J.R., Dooley,J.S.G., Rooney,P.J.,	
Matsuda,M. and Moore,J.E.	
Cryptosporidium parvum 18S rRNA partial gene sequence	
Unpublished	
2 (bases 1 to 413)	
Finn,M.B., Lowery,C.J., Nagano,Y., Moore,J.E. and Dooley,J.S.G.	
Direct Submission	
Submitted (18-DEC-2003) Department of Bacteriology, Northern	
Ireland Public Health Laboratory, Belfast City Hospital, Lisburn	
Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK	
Location/Qualifiers	
source	
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/mol_type="genomic DNA"	
/strain="Fox3"	
/isolation_source="fecal material from a fox"	
/db_xref="taxon:5807"	
/country="Ireland"	
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rRNA	
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Best Local Similarity	100.0%; Pred. No. 7.9;
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCGTAAAGTTATTATGAGTCACC 23 
Db	30 CCGTAAAGTTATTATGAGTCACC 8 
RESULT 6	
AY508963/c	
LOCUS	AY508963 415 bp DNA linear INV 25-FEB-2004
DEFINITION	Cryptosporidium parvum strain Fox8 18S ribosomal RNA gene, partial sequence.
ACCESSION	AY508963
VERSION	AY508963.1 GI:42716334
KEYWORDS	.
SOURCE	Cryptosporidium parvum
ORGANISM	Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;	
Cryptosporidiidae; Cryptosporidium.	
1 (bases 1 to 415)	
Nagano,Y., Finn,M.B., Lowery,C.J., Murphy,T., McCorry,K.A.,	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	
1. .23	



Crothers,E., Watabe,M., Rao,J.R., Dooley,J.S.G., Rooney,P.J., Matsuda,M. and Moore,J.E.  
Cryptosporidium parvum 18S rRNA partial gene sequence  
Unpublished  
2 (bases 1 to 415)  
Finn,M.B., Lowery,C.J., Nagano,Y., Moore,J.E. and Dooley,J.S.G.  
Direct Submission  
Submitted (18-DEC-2003) Department of Bacteriology, Northern Ireland Public Health Laboratory, Belfast City Hospital, Lisburn Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK  
Location/Qualifiers  
1. .415  
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Cryptosporidiidae; Cryptosporidium.  
1 (bases 1 to 600)  
Xiao,L., Alderisio,K., Limor,J., Royer,M. and Lal,A.A.  
Identification of species and sources of Cryptosporidium oocysts in storm waters with a small-subunit rRNA-based diagnostic and genotyping tool  
Appl. Environ. Microbiol. 66 (12), 5492-5498 (2000)  
11097935  
2 (bases 1 to 600)  
Xiao,L., Alderisio,K., Limor,J.R., Royer,M. and Lal,A.A.  
Direct Submission  
Submitted (02-MAY-2000) Division of Parasitic Diseases, Centers for Disease Control and Prevention, 4770 Buford Highway, F-12, Chamblee, GA 30341, USA  
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Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.  
1 (bases 1 to 646)  
Azadpour-Keeley,A. and Caldwell,M.  
Evaluation of Cryptosporidium oocysts and Giardia cysts in a watershed reservoir  
Unpublished  
2 (bases 1 to 646)  
Azadpour-Keeley,A.  
Direct Submission  
Submitted (11-APR-2005) EPA/ORD/NRMRL, GWERD, 919 Kerr Research Dr., Ada, OK 74820, USA  
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Db 61 CCGTAAAGTTATTATGAGTCACC 39  
  
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DEFINITION  
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VERSION  
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Cryptosporidium sp. BDI  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.  
1 (bases 1 to 660)  
Morgan,U.M., Monis,P.T., Xiao,L., Limor,J., Sulaiman,I., Raidal,S., O'Donoghue,P., Gasser,R., Murray,A., Fayer,R., Blagburn,B.L., Lal,A.A. and Thompson,A.R.C.  
Molecular and phylogenetic characterisation of Cryptosporidium from birds  
Int. J. Parasitol. 31 (3), 289-296 (2001)  
11226456  
2 (bases 1 to 660)  
Morgan,U.M., Monis,P.T. and Xiao,L.  
Direct Submission  
Submitted (26-OCT-2000) Division of Veterinary and Biomedical Science, Murdoch University, Murdoch Drive, Perth, WA 6150, Australia  
Location/Qualifiers  
  
FEATURES

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rRNA

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Db 213 CCGTAAAGTTATTATGAGTCACC 191

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LOCUS AF316631 665 bp DNA linear INV 30-MAR-2001  
DEFINITION Cryptosporidium sp. Q1 18S ribosomal RNA gene, partial sequence.  
ACCESSION AF316631  
VERSION AF316631.1 GI:12744418  
KEYWORDS  
SOURCE Cryptosporidium sp. Q1  
ORGANISM Cryptosporidium sp. Q1  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.  
REFERENCE 1 (bases 1 to 665)  
AUTHORS Morgan,U.M., Monis,P.T., Xiao,L., Limor,J., Sulaiman,I., Raidal,S., O'Donoghue,P., Gasser,R., Murray,A., Fayer,R., Blagburn,B.L., Lal,A.A. and Thompson,A.R.C.  
TITLE Molecular and phylogenetic characterisation of Cryptosporidium from birds  
JOURNAL Int. J. Parasitol. 31 (3), 289-296 (2001)  
PUBMED 11226456  
REFERENCE 2 (bases 1 to 665)  
AUTHORS Morgan,U.M., Monis,P.T. and Xiao,L.  
TITLE Direct Submission  
JOURNAL Submitted (26-OCT-2000) Division of Veterinary and Biomedical Science, Murdoch University, Murdoch Drive, Perth, WA 6150, Australia  
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rRNA

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CP18RRNA1/c  
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DEFINITION Cryptosporidium parvum 18S ribosomal RNA gene, partial sequence.  
ACCESSION AF162429  
VERSION AF162429.1 GI:5916184  
KEYWORDS  
SEGMENT 1 of 2  
SOURCE Cryptosporidium parvum

ORGANISM Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.  
REFERENCE 1 (bases 1 to 704)  
AUTHORS Blears,M.J., Pokorny,N.J., Carreno,R.A., Chen,S., De Grandis,S.A., Lee,H. and Trevors,J.T.  
TITLE DNA fingerprinting of Cryptosporidium parvum isolates using amplified fragment length polymorphism (AFLP)  
JOURNAL J. Parasitol. 86 (4), 838-841 (2000)  
PUBMED 10958466  
REFERENCE 2 (bases 1 to 704)  
AUTHORS Pokorny,N.J.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUN-1999) Environmental Biology, University of Guelph, Edmund C. Bovey Building, Guelph, ON N1G 2W1, Canada  
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source Location/Qualifiers  
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LOCUS DQ067569 712 bp DNA linear INV 18-JUN-2005  
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VERSION DQ067569.1 GI:67527112  
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SOURCE Cryptosporidium parvum  
ORGANISM Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.  
REFERENCE 1 (bases 1 to 712)  
AUTHORS Kang,G., Dheepa,M., Jayandhran,B., Ramani,S. and Ward,H.D.  
TITLE Multi-locus genotyping of Cryptosporidium species from HIV-infected individuals with and without diarrhea in southern India  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 712)  
AUTHORS Kang,G., M.D., Jayandhran,B., Ramani,S. and Ward,H.D.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAY-2005) GI Sciences, Christian Medical College, Ida Scudder Road, Vellore, TN 632004, India  
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rRNA

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Db 29 CCGTAAAGTTATTATGAGTCACC 7

RESULT 13  
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ACCESSION  
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VERSION  
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KEYWORDS  
SOURCE  
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ORGANISM  
Cryptosporidium sp.  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporidiidae; Cryptosporidium.  
REFERENCE  
1 (bases 1 to 715)  
Xiao,L., Alderisio,K., Limor,J., Royer,M. and Lal,A.A.  
AUTHORS  
Identification of species and sources of Cryptosporidium oocysts in storm waters with a small-subunit rRNA-based diagnostic and genotyping tool  
TITLE  
Appl. Environ. Microbiol. 66 (12), 5492-5498 (2000)  
JOURNAL  
PUBMED  
11097935  
REFERENCE  
2 (bases 1 to 715)  
Xiao,L., Alderisio,K., Limor,J.R., Royer,M. and Lal,A.A.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (02-MAY-2000) Division of Parasitic Diseases, Centers for Disease Control and Prevention, 4770 Buford Highway, F-12, Chamblee, GA 30341, USA  
JOURNAL

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VERSION  
AY268582.1 GI:33347884  
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SOURCE  
Cryptosporidium parvum  
ORGANISM  
Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporidiidae; Cryptosporidium.  
REFERENCE  
1 (bases 1 to 744)  
Xiao,L., Ryan,U.M., Graczyk,T.K., Limor,J., Li,L., Kombert,M., Junge,R., Sulaiman,I.M., Zhou,L., Arrowood,M.J., Koudela,B., Modry,D. and Lal,A.A.  
AUTHORS  
Genetic diversity of Cryptosporidium spp. in captive reptiles  
TITLE  
Appl. Environ. Microbiol. 70 (2), 891-899 (2004)  
PUBMED  
14766569  
Xiao,L.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (07-APR-2003) CDC, DPD/NCID, 4770 Buford Hwy, Atlanta, GA

30341, USA  
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Location/Qualifiers  
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporidiidae; Cryptosporidium.  
REFERENCE  
1 (bases 1 to 748)  
Xiao,L., Ryan,U.M., Graczyk,T.K., Limor,J., Li,L., Kombert,M., Junge,R., Sulaiman,I.M., Zhou,L., Arrowood,M.J., Koudela,B., Modry,D. and Lal,A.A.  
AUTHORS  
Genetic diversity of Cryptosporidium spp. in captive reptiles  
TITLE  
Appl. Environ. Microbiol. 70 (2), 891-899 (2004)  
PUBMED  
14766569  
Xiao,L.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (07-APR-2003) CDC, DPD/NCID, 4770 Buford Hwy, Atlanta, GA

30341, USA  
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Location/Qualifiers  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
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Perfect score: 23  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues  
Total number of hits satisfying chosen parameters: 9993994

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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9: Geneseqn2003bs:\*  
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11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	23	100.0	23	6 AAD38439	Aad38439 Cryptospo
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C 4	23	100.0	23	6 AAD38433	Aad38433 Cryptospo
C 5	23	100.0	1750	2 AAT90818	Aat90818 C. parvum
C 6	23	100.0	1750	3 AAA46368	Aaa46368 Nucleotid
C 7	18.8	81.7	447	2 AAQ71867	Aaq71867 G. vesicu
C 8	18.8	81.7	447	2 AAQ71870	Aaq71870 E. pisifo
C 9	18.8	81.7	447	2 AAQ71868	Aaq71868 G. intrar
C 10	18.8	81.7	512	8 ABZ56146	Abz56146 Aspergill
C 11	18.8	81.7	568	3 AAF11545	Aaf11545 Aspergill
C 12	18.8	81.7	568	13 ADU55586	Adu55586 Aspergill
C 13	18.8	81.7	568	14 ADZ93589	Adz93589 Aspergill
C 14	18.8	81.7	1024	3 AAF11316	Aaf11316 Aspergill
C 15	18.8	81.7	1024	13 ADU55357	Adu55357 Aspergill
C 16	18.8	81.7	1024	14 ADZ93360	Adz93360 Aspergill
C 17	18.8	81.7	1228	10 ABZ80030	Abz80030 Xylariale
C 18	18.8	81.7	1731	4 AAI68286	Aai68286 Bulgaria
C 19	18.8	81.7	1731	13 ADP79725	Adp79725 Anti-tumo

C 20	18.8	81.7	1733	2 AAZ00859	Aaz00859 A. fumiga
C 21	18.8	81.7	1733	13 ADP79724	Adp79724 Anti-tumo
C 22	18.8	81.7	2055	8 ABZ20766	Abz20766 Muscodor
C 23	18.8	81.7	2055	14 ADW88676	Adw88676 Muscodor
C 24	18.8	81.7	2089	8 ABZ20764	Abz20764 Muscodor
C 25	18.8	81.7	2089	14 ADW88674	Adw88674 Muscodor
C 26	18.2	79.1	433	12 ADN38639	Adn38639 DNA fragm
C 27	18.2	79.1	709	2 ADR01589	Adr01589 A. gossyp
C 28	17.8	77.4	1101	12 ADO10084	Ado10084 Novel hum
C 29	17.8	77.4	1102	6 ABQ93901	Abq93901 Human pro
C 30	17.8	77.4	1102	6 ABQ93902	Abq93902 Human pro
C 31	17.8	77.4	1102	12 ADO10082	Ado10082 Novel hum
C 32	17.2	74.8	444	2 AAQ71869	Aaq71869 G. margar
C 33	17.2	74.8	703	2 ADR01486	Adr01486 A. gossyp
C 34	17.2	74.8	723	2 ADR02260	Adr02260 A. gossyp
C 35	17.2	74.8	1732	12 ADH43081	Adh43081 18S rRNA
C 36	17.2	74.8	1734	5 ABK49559	Abk49559 Putrefact
C 37	17.2	74.8	1737	8 AAL51417	Aal51417 Spongipel
C 38	17.2	74.8	1740	11 ADZ11851	Adz11851 Candida a
C 39	17.2	74.8	1743	11 ADZ11854	Adz11854 Geotrichu
C 40	17.2	74.8	1764	14 ADV14619	Adv14619 Issatchen
C 41	17.2	74.8	1776	4 AAF25849	Aaf25849 S. exiguu
C 42	17.2	74.8	1793	2 AAV60107	Aav60107 Rhizocton
C 43	17.2	74.8	1798	4 AAD14297	Aad14297 Yeast DNA
C 44	17.2	74.8	1798	5 AAD14004	Aad14004 DNA to in
C 45	17.2	74.8	1798	13 ADR32081	Adr32081 Genomic r

ALIGNMENTS

RESULT 1  
AAD38427/c  
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AC AAD38427;  
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DT 10-SEP-2002 (first entry)  
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DE Cryptosporidium sp. target DNA #9.  
XX  
KW Hybridisation; amplification; detection; ds.  
XX  
OS Cryptosporidium sp.  
XX  
PN WO200222890-A2.  
XX  
PD 21-MAR-2002.  
XX  
PF 11-SEP-2001; 2001WO-US042192.  
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PR 12-SEP-2000; 2000US-0232028P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Cunningham MM, Stull PD, Weisburg WG;  
XX  
DR WPI; 2002-454395/48.  
XX  
PT Novel oligonucleotides functioning as hybridization probes, helper probes and/or primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms, useful for detecting the organism in a test sample.  
XX  
PS Claim 23; Page 8; 133pp; English.  
XX  
CC The invention relates to oligonucleotides functioning as hybridisation assay probes, helper probes and/or amplification primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms. Probes and primers of the invention are useful for detecting the presence of Cryptosporidium organisms in general and C. parvum organisms in particular in a test sample. The present sequence is Cryptosporidium sp. target DNA

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SQ Sequence 23 BP; 7 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

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Db      23 CCGTAAAGTTATTATGAGTCACC 1

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DT      10-SEP-2002 (first entry)
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KW      Hybridisation; amplification; detection; ds.
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AC      AAD38445;
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DT      10-SEP-2002 (first entry)
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PF      11-SEP-2001; 2001WO-US042192.
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PR      12-SEP-2000; 2000US-0232028P.
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PA      (GENP-) GEN-PROBE INC.
XX
PI      Cunningham MM, Stull PD, Weisburg WG;
XX
DR      WPI; 2002-454395/48.
XX
PT      Novel oligonucleotides functioning as hybridization probes, helper probes
PT      and/or primers, targeted to nucleic acid sequences derived from
PT      Cryptosporidium organisms, useful for detecting the organism in a test
PT      sample.
XX
PS      Claim 23; Page 8; 133pp; English.
XX
CC      The invention relates to oligonucleotides functioning as hybridisation
CC      assay probes, helper probes and/or amplification primers, targeted to
CC      nucleic acid sequences derived from Cryptosporidium organisms. Probes and
CC      primers of the invention are useful for detecting the presence of
CC      Cryptosporidium organisms in general and C. parvum organisms in
CC      particular in a test sample. The present sequence is Cryptosporidium sp.
CC      target RNA
XX
SQ      Sequence 23 BP; 7 A; 5 C; 4 G; 0 T; 7 U; 0 Other;

Query Match      100.0%; Score 23; DB 6; Length 23;
Best Local Similarity 69.6%; Pred. No. 0.56;
Matches 16; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGTAAAGTTATTATGAGTCACC 23
Db      1 CCGUAAAGUUUAUGAGUCACC 23

RESULT 4
AAD38433/c
ID      AAD38433 standard; RNA; 23 BP.
XX
AC      AAD38433;
XX
DT      10-SEP-2002 (first entry)
XX
DE      Cryptosporidium sp. target RNA #9.
XX
KW      Hybridisation; amplification; detection; ss.
XX
OS      Cryptosporidium sp.
XX
PN      WO200222890-A2.
XX
PD      21-MAR-2002.
XX
PF      11-SEP-2001; 2001WO-US042192.
XX
PR      12-SEP-2000; 2000US-0232028P.
XX
PA      (GENP-) GEN-PROBE INC.
XX
PI      Cunningham MM, Stull PD, Weisburg WG;
XX
```



DR WPI; 2002-454395/48.

XX Novel oligonucleotides functioning as hybridization probes, helper probes

PT and/or primers, targeted to nucleic acid sequences derived from

PT Cryptosporidium organisms, useful for detecting the organism in a test

PT sample.

XX Claim 23; Page 8; 133pp; English.

PS

XX The invention relates to oligonucleotides functioning as hybridisation

CC assay probes, helper probes and/or amplification primers, targetted to

CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and

CC primers of the invention are useful for detecting the presence of

CC Cryptosporidium organisms in general and C. parvum organisms in

CC particular in a test sample. The present sequence is Cryptosporidium sp.

CC target RNA

XX

SQ Sequence 23 BP; 7 A; 4 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23

Db 23 CCGTAAAGTTATTATGAGTCACC 1

RESULT 5

AAT90818/c

ID AAT90818 standard; DNA; 1750 BP.

XX

AC AAT90818;

XX

DT 22-APR-1998 (first entry)

XX

DE C. parvum 18S rRNA gene.

XX

KW PCR primer; amplify; C. parvum; 18S rRNA gene; forensic analysis;

KW microorganism classification; target nucleic acid sequence segregation;

KW genetic abnormality identification; inborn error of metabolism;

KW infectious disease diagnosis; ss.

XX

OS Cryptosporidium parvum.

XX

PN WO9735026-A1.

XX

PD 25-SEP-1997.

XX

PF 17-MAR-1997; 97WO-US004170.

XX

PR 18-MAR-1996; 96US-00617045.

XX

PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.

PI Wick JF, Mueller R, Blassak ML, Wilkosz RK;

XX WPI; 1997-480231/44.

DR

XX Segregating copy of target nucleic acid sequence found in single stranded

PT polynucleotide - by serial generation of double stranded DNA containing

PT extended terminal nicking sites, to displace any existing

PT polynucleotide(s).

XX

PS Disclosure; Page 60-62; 92pp; English.

XX

CC This sequence represents the C. parvum 18S rRNA gene which can be

CC isolated using the sequences represented by AAT90815-T90817 in the method

CC of the invention. The method is for segregating a copy of a target

CC nucleic acid sequence (I) found in a single stranded polynucleotide (II),

CC which is suitable for use in amplifying (I). The methods for the

CC amplification, detection and quantification of specific (I) can be used

CC in microorganism classification, identification of genetic abnormalities

CC including inborn errors of metabolism, diagnosis of infectious diseases,

CC forensic analysis, environmental resting and studies involving

CC developmental and cellular biology. The methods are versatile, reliable

CC and simple and are capable of amplifying both RNA and DNA, and should do

CC so exponentially, using a minimum number of primers under substantially

CC isostatic conditions

XX

SQ Sequence 1750 BP; 533 A; 292 C; 390 G; 535 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 2; Length 1750;

Best Local Similarity 100.0%; Pred. No. 0.65;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23

Db 254 CCGTAAAGTTATTATGAGTCACC 232

RESULT 6

AAA46368/c

ID AAA46368 standard; DNA; 1750 BP.

XX

AC AAA46368;

XX

DT 04-SEP-2000 (first entry)

XX

DE Nucleotide sequence of the 18S ribosomal DNA of C. parvum.

XX

KW Isothermal amplification; hemi-modified restriction endonuclease;

KW restriction endonuclease; 18S ribosomal DNA; ss.

XX

OS Cryptosporidium parvum.

XX

PN WO200028084-A1.

XX

PD 18-MAY-2000.

XX

PF 05-NOV-1999; 99WO-US025927.

XX

PR 06-NOV-1998; 98US-00186910.

XX

PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.

XX

PI Jolly JF;

XX

DR WPI; 2000-376589/32.

XX

PT Isothermal method for amplifying a target nucleic acid, with improved

PT thermodynamics and kinetics over prior art methods.

XX

PS Example 1; Page 47-49; 64pp; English.

XX

CC The specification describes an isothermal target nucleic acid

CC amplification method. The method comprises contacting a mixture of a

CC target, two primers containing hemi-modified restriction endonuclease

CC sites and modified nucleotides capable of forming phosphodiester bonds,

CC and a polymerase lacking 5' to 3' exonuclease activity, with a

CC restriction endonuclease, and incubating under isothermal conditions. The

CC method can be used for amplifying nucleotide sequences. The method

CC exhibits improved thermodynamics and kinetics, resulting in increased

CC sensitivity and polynucleotide length, thus broadening both the range of

CC target sources and the range of target lengths. The present sequence

CC represents the 18S ribosomal DNA of C. parvum, and contains a RNA target

CC (nucleotides 937-1095) which is used to demonstrate the method of the

CC invention

XX

SQ Sequence 1750 BP; 533 A; 292 C; 390 G; 535 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 3; Length 1750;

Best Local Similarity 100.0%; Pred. No. 0.65;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23

```
Db      254 CCGTAAAGTTATTATGAGTCACC 232
|||||
RESULT 7
AAQ71867/c
ID  AAQ71867 standard; DNA; 447 BP.
XX
XX
AC  AAQ71867;
XX
XX  23-MAR-1995 (first entry)
XX
DE  G. vesiculiferum small ribosomal subunit RNA.
XX
KW  Nuclear 18S ribosomal gene; SSU; probe; primer;
KW  arbuscular endomycorrhizal fungi; plant; root; ds.
XX
OS  Glomus vesiculiferum.
XX
PN  CA2086136-A.
XX
XX  24-JUN-1994.
XX
PF  23-DEC-1992; 92CA-02086136.
XX
PR  23-DEC-1992; 92CA-02086136.
XX
PA  (SIMO/) SIMON L.
XX
XX  Simon L, Lalonde M;
PI
XX  WPI; 1994-264577/33.
XX
PT  New oligonucleotide probes - used for the detection of arbuscular
PT  endomycorrhizal fungi in plant root samples.
XX
PS  Disclosure; Page 18; 40pp; English.
XX
CC  The gene sequence of the small ribosomal subunit RNA of arbuscular
CC  endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
CC  intraradices and Gigaspora margarita were compared with that of a non-
CC  arbuscular endomycorrhizal fungus, Endogone pisiiformis, in order to
CC  design taxon specific primers/probes
XX
SQ  Sequence 447 BP; 135 A; 86 C; 107 G; 118 T; 0 U; 1 Other;

Query Match      81.7%; Score 18.8; DB 2; Length 447;
Best Local Similarity 90.9%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      158 CGAAAAGTTATTATGAATCACC 137
|||||

RESULT 8
AAQ71870/c
ID  AAQ71870 standard; DNA; 447 BP.
XX
XX
AC  AAQ71870;
XX
XX  23-MAR-1995 (first entry)
XX
DE  E. pisiiformis small ribosomal subunit RNA.
XX
KW  Nuclear 18S ribosomal gene; SSU; probe; primer;
KW  arbuscular endomycorrhizal fungi; plant; root; ds.
XX
OS  Endogone pisiiformis.
XX
FH  Key Location/Qualifiers
FT  misc_difference 116..135
FT  /*tag= a
```

```
FT
XX
PN  CA2086136-A.
XX
PD  24-JUN-1994.
XX
PF  23-DEC-1992; 92CA-02086136.
XX
PR  23-DEC-1992; 92CA-02086136.
XX
PA  (SIMO/) SIMON L.
XX
XX  Simon L, Lalonde M;
PI
XX  WPI; 1994-264577/33.
XX
DR  New oligonucleotide probes - used for the detection of arbuscular
XX  endomycorrhizal fungi in plant root samples.
PT
XX
PS  Disclosure; Page 20; 40pp; English.
XX
CC  The gene sequence of the small ribosomal subunit RNA of arbuscular
CC  endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
CC  intraradices and Gigaspora margarita were compared with that of a non-
CC  arbuscular endomycorrhizal fungus, Endogone pisiiformis, in order to
CC  design taxon specific primers/probes
XX
SQ  Sequence 447 BP; 133 A; 77 C; 100 G; 117 T; 0 U; 20 Other;

Query Match      81.7%; Score 18.8; DB 2; Length 447;
Best Local Similarity 90.9%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      158 CGAAAAGTTATTATGAATCACC 137
|||||

RESULT 9
AAQ71868/c
ID  AAQ71868 standard; DNA; 447 BP.
XX
AC  AAQ71868;
XX
XX  23-MAR-1995 (first entry)
XX
DE  G. intraradices small ribosomal subunit RNA.
XX
KW  Nuclear 18S ribosomal gene; SSU; probe; primer;
KW  arbuscular endomycorrhizal fungi; plant; root; ds.
XX
OS  Glomus intraradices.
XX
PN  CA2086136-A.
XX
XX  24-JUN-1994.
XX
PF  23-DEC-1992; 92CA-02086136.
XX
PR  23-DEC-1992; 92CA-02086136.
XX
PA  (SIMO/) SIMON L.
XX
XX  Simon L, Lalonde M;
PI
XX  WPI; 1994-264577/33.
XX
XX  New oligonucleotide probes - used for the detection of arbuscular
PT  endomycorrhizal fungi in plant root samples.
XX
PS  Disclosure; Page 19; 40pp; English.
XX
CC  The gene sequence of the small ribosomal subunit RNA of arbuscular
```

CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus  
CC intraradices and Gigaspora margarita were compared with that of a non-  
CC arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to  
CC design taxon specific primers/probes  
XX  
SQ Sequence 447 BP; 137 A; 86 C; 107 G; 117 T; 0 U; 0 Other;  
Query Match 81.7%; Score 18.8; DB 2; Length 447;  
Best Local Similarity 90.9%; Pred. No. 57;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CGTAAAGTTATTATGATCACC 23  
DB 158 CGAAAAGTTATTATGAATCACC 137  
RESULT 10  
ABZ56146/C  
ID ABZ56146 standard; cDNA; 512 BP.  
XX  
AC ABZ56146;  
XX  
DT 28-MAR-2003 (first entry)  
XX  
DE Aspergillus oryzae polynucleotide SEQ ID NO 5259.  
XX  
KW Aspergillus oryzae; fermentation; fungus; industrial; EST;  
KW expressed sequence tag; gene; ss.  
XX  
OS Aspergillus oryzae.  
XX  
PN WO200279476-A1.  
XX  
PD 10-OCT-2002.  
XX  
PF 22-MAR-2002; 2002WO-IB000890.  
XX  
PR 30-MAR-2001; 2001JP-00098371.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (NARE-) NAT RES INST BREWING.  
PA (NORQ) NAT FOOD RES INST MIN AGRIC.  
XX  
PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;  
PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;  
XX  
DR WPI; 2003-046817/04.  
XX  
PT Detection of expression of specific Aspergillus genes for monitoring the  
PT fermentation and growth conditions of the fungus, using DNA probes.  
XX  
PS Claim 1; SEQ ID NO 5259; 48pp + Sequence Listing; Japanese.  
XX  
CC The invention relates to a polynucleotide having any of 6006 specific  
CC sequences (ABZ50888-ABZ56893), which are expressed by a fungus under  
CC specific culture conditions including one or more of eutrophic,  
CC oligotrophic, solid, early germination, alkaline, high temperature, low  
CC temperature or maltose culture or polynucleotides stringently hybridising  
CC to these sequences. The polynucleotides are useful for monitoring the  
CC progress of fermentation and the growth conditions of a fungus,  
CC especially of Aspergillus oryzae which is widely used in industrial  
CC fermentation. Also monitoring for fungal contamination. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 512 BP; 150 A; 105 C; 123 G; 134 T; 0 U; 0 Other;  
Query Match 81.7%; Score 18.8; DB 8; Length 512;  
Best Local Similarity 90.9%; Pred. No. 57;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CGTAAAGTTATTATGATCACC 23

Db 227 CGTTAAGTTATTATGAATCACC 206  
RESULT 11  
AAF11545/C  
ID AAF11545 standard; cDNA; 568 BP.  
XX  
AC AAF11545;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Aspergillus niger EST SEQ ID NO:4068.  
XX  
KW Multiple gene expression; filamentous fungal cell; EST;  
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
KW culture condition; environmental stress; spore morphogenesis;  
KW metabolic pathway engineering; catabolic pathway engineering; ss.  
XX  
OS Aspergillus niger.  
XX  
PN WO200056762-A2.  
XX  
PD 28-SEP-2000.  
XX  
PF 22-MAR-2000; 2000WO-US007781.  
XX  
PR 22-MAR-1999; 99US-00273623.  
XX  
PA (NOVO) NOVO NORDISK BIOTECH INC.  
PA (NOVO) NOVO NORDISK AS.  
XX  
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
XX  
DR WPI; 2000-594572/56.  
XX  
PT Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags.  
XX  
PS Claim 87; Page 1791-1792; 3161pp; English.  
XX  
CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring the  
CC global expression of genes from FF cells allows the production potential  
CC of the microorganisms to be improved. New genes may be discovered,  
CC possible functions of unknown open reading frames can be identified and  
CC gene copy number variation and stability can be monitored. The expression  
CC of genes can be used to study how FF cells adapt to changes in culture  
CC conditions, environmental stress, spore morphogenesis, recombination,  
CC metabolic or catabolic pathway engineering. Using ESTs provides several  
CC advantages over genomic or random cDNA clones including elimination of  
CC redundancy as one spot on an array equals one gene or open reading frame,  
CC and organisation of the microarrays based on function of the gene  
CC products to facilitate analysis of the results. AAF07478 to AAF11247  
CC represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents  
CC ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from  
CC Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from  
CC Trichoderma reesei, which are all specifically claimed in the present  
CC invention  
XX  
SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 0 U; 6 Other;  
Query Match 81.7%; Score 18.8; DB 3; Length 568;  
Best Local Similarity 90.9%; Pred. No. 58;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
||| ||||| ||||| ||||| |||||  
Db 249 CGTTAAGTTATTATGATTCACC 228

RESULT 12  
ADU55586/c  
ID ADU55586 standard; cDNA; 568 BP.  
XX  
AC ADU55586;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Aspergillus niger strain Bo-95 EST, SEQ ID NO:4068.  
XX  
KW Gene expression; biochip; microarray; hybridization; EST;  
KW expressed sequence tag; ss.  
XX  
OS Aspergillus niger; strain Bo-95.  
XX  
PN US2004229367-A1.  
PD  
PD 18-NOV-2004.  
XX  
PF 29-AUG-2003; 2003US-00653047.  
XX  
PR 22-MAR-1999; 99US-00273623.  
PR 22-MAR-2000; 2000US-00533559.  
XX  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES INC AS.  
XX  
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
XX WPI; 2004-832481/82.  
DR  
XX  
PT Monitoring differential expression of genes in a filamentous fungal cell  
PT relative to expression of the genes in second filamentous fungal cells,  
PT comprises using microarrays containing Fusarium venenatum expressed  
PT sequence tags.  
XX  
PS Example 11; SEQ ID NO 4068; 274pp; English.  
XX

The invention relates to a method for monitoring the differential  
expression of genes in a first filamentous fungal cell relative to the  
same genes in one or more second filamentous fungal cells. The method  
involves differentially labeling nucleic acids from the first and second  
fungal cells with fluorescent reporter dyes, and adding the mixture of  
fluorescently labeled polynucleotides to a substrate containing an array  
of Fusarium venenatum expressed sequence tags (ESTs) selected from  
ADU51519-ADU55288 under conditions that permit hybridization. Relative  
expression of genes in the fungal cells is determined by fluorescence;  
the fluorescent signal emitted when labeled nucleic acids from the first  
fungal cell bind to the ESTs in the array differs in color from that  
emitted when labeled nucleic acids from the second fungal cell hybridise.  
When both sets of labeled nucleic acids bind to the array, a distinct  
combined fluorescence emission color is produced. The filamentous fungal  
cells used in the method are chosen from Acremonium, Aspergillus,  
Fusarium, Humicola, Mucor, Myceliophthora, Neurospora, Penicillium,  
Thielavia, Tolypocladium, and Trichoderma cells, preferably Fusarium  
venenatum, Aspergillus niger, or Aspergillus oryzae. The method of the  
invention is useful for monitoring the expression of a plurality of genes  
in filamentous fungal cells, in order to improve the cells' protein  
production capacity when such organisms are used for the industrial  
production of proteins (e.g., enzymes). Sequences ADU55289-ADU55894  
represent ESTs derived from Aspergillus niger strain Bo-95 which were  
obtained in an example of the invention. Note: The sequence data for this  
patent did not form part of the printed specification, but was obtained  
in electronic format directly from the US patent office at  
seqdata.uspto.gov/sequence.html?DocID=US20040222367.

XX Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 0 U; 6 Other;

Query Match 81.7%; Score 18.8; DB 13; Length 568;  
Best Local Similarity 90.9%; Pred. No. 58;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
||| ||||| ||||| ||||| |||||  
Db 249 CGTTAAGTTATTATGATTCACC 228

RESULT 13  
ADZ93589/c  
ID ADZ93589 standard; cDNA; 568 BP.  
XX  
AC ADZ93589;  
XX  
DT 11-AUG-2005 (first entry)  
XX  
DE Aspergillus niger expressed sequence tag cDNA SEQ ID NO 4068.  
XX  
KW differential expression; gene expression; filamentous fungus;  
KW expressed sequence tag; EST; variation; microarray; ss.  
XX  
OS Aspergillus niger.  
XX  
PN US6902887-B1.  
PD  
PD 07-JUN-2005.  
XX  
PF 22-MAR-2000; 2000US-00533559.  
XX  
PR 22-MAR-1999; 99US-00273623.  
XX  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES AS.  
XX  
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
XX WPI; 2005-401635/41.  
DR  
XX  
PT Monitoring differential expression of genes in first filamentous fungal  
PT cell relative to that of genes in second fungal cells, comprises  
PT hybridizing fluorescence labeled nucleic acids from the cells to an array  
PT of expressed sequence tags.  
XX  
PS Disclosure; SEQ ID NO 4068; 264pp; English.  
XX

The invention relates to a method of monitoring (M1) differential  
expression of multiple genes in a first filamentous fungal cell relative  
to expression of the same genes in one or more second filamentous fungal  
cells, comprises adding fluorescence labeled nucleic acids isolated from  
the cells to a substrate containing an array of Aspergillus oryzae  
expressed sequence tag (EST) of ADZ93898-ADZ96922, and examining the  
array under fluorescence excitation conditions. (M1) is useful for  
monitoring global expression of several genes from a filamentous fungal  
cell, discovering new genes, identifying possible functions of unknown  
open reading frames and monitoring gene copy number variation and  
stability. In (M1), one spot on an array equals one gene or open reading  
frame, extensive follow-up characterization is unnecessary since sequence  
information is available and EST microarrays can be organized based on  
function of the gene products. This sequence corresponds to an EST  
sequence of the invention. (Note: this sequence is not given in the  
printed specification but can be obtained in electronic form from the  
USPTO web site seqdata.uspto.gov/sequence.html; Document ID: 6902887B1).

XX Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 0 U; 6 Other;

Query Match 81.7%; Score 18.8; DB 14; Length 568;  
Best Local Similarity 90.9%; Pred. No. 58;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
||| ||||| ||||| ||||| |||||



Db	249	CGTTAAGTTATTATGATTCACC	228
RESULT 14			
AAAF11316/C			
ID	AAAF11316	standard; cDNA; 1024 BP.	
XX	AAAF11316;		
AC			
XX	13-MAR-2001	(first entry)	
DT			
XX	Aspergillus niger	EST SEQ ID NO:3839.	
DE			
XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.		
KW			
OS	Aspergillus niger.		
XX			
PN	WO200056762-A2.		
XX			
PD	28-SEP-2000.		
XX			
PF	22-MAR-2000;	2000WO-US007781.	
XX			
PR	22-MAR-1999;	99US-00273623.	
XX			
PA	(NOVO )	NOVO NORDISK BIOTECH INC.	
PA	(NOVO )	NOVO NORDISK AS.	
XX			
PI	Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;		
XX			
DR	WPI; 2000-594572/56.		
XX			
PT	Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags.		
PT			
XX			
PS	Claim 87; Page 1718; 3161pp; English.		
XX			
CC	The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAFO7478 to AAFA11247 represents ESTs from Fusarium venenatum; AAFA11248 to AAFA11853 represents ESTs from Aspergillus niger; AAFA11854 to AAFA14878 represents ESTs from Aspergillus oryzae; and AAFA14879 to AAFA15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention		
XX			
SQ	Sequence 1024 BP; 275 A; 204 C; 275 G; 269 T; 0 U; 1 Other;		
Query Match 81.7%; Score 18.8; DB 3; Length 1024;			
Best Local Similarity 90.9%; Pred. No. 59;			
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	2	CGTAAAGTTATTATGAGTCACC	23
Db	57	CGTTAAGTTATTATGATTCACC	36
RESULT 15			
ADU55357/C			
ID	ADU55357	standard; cDNA; 1024 BP.	
XX			
AC	ADU55357;		
XX			
DT	10-FEB-2005	(first entry)	
XX			
DE	Aspergillus niger	strain Bo-95 EST, SEQ ID NO:3839.	
XX			
KW	Gene expression; biochip; microarray; hybridization; EST; expressed sequence tag; ss.		
KW			
XX	Aspergillus niger; strain Bo-95.		
OS			
XX			
PN	US2004229367-A1.		
XX			
PD	18-NOV-2004.		
XX			
PF	29-AUG-2003;	2003US-00653047.	
XX			
PR	22-MAR-1999;	99US-00273623.	
PR	22-MAR-2000;	2000US-00533559.	
XX			
PA	(NOVO )	NOVOZYMES BIOTECH INC.	
PA	(NOVO )	NOVOZYMES INC AS.	
XX			
PI	Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;		
XX			
DR	WPI; 2004-832481/82.		
XX			
PT	Monitoring differential expression of genes in a filamentous fungal cell relative to expression of the genes in second filamentous fungal cells, comprises using microarrays containing Fusarium venenatum expressed sequence tags.		
PT			
XX			
PS	Example 11; SEQ ID NO 3839; 274pp; English.		
XX			
CC	The invention relates to a method for monitoring the differential expression of genes in a first filamentous fungal cell relative to the same genes in one or more second filamentous fungal cells. The method involves differentially labeling nucleic acids from the first and second fungal cells with fluorescent reporter dyes, and adding the mixture of fluorescently labeled polynucleotides to a substrate containing an array of Fusarium venenatum expressed sequence tags (ESTs) selected from ADU51519-ADU55288 under conditions that permit hybridization. Relative expression of genes in the fungal cells is determined by fluorescence; the fluorescent signal emitted when labeled nucleic acids from the first fungal cell bind to the ESTs in the array differs in color from the first emitted when labeled nucleic acids from the second fungal cell hybridise. When both sets of labeled nucleic acids bind to the array, a distinct combined fluorescence emission color is produced. The filamentous fungal cells used in the method are chosen from Acremonium, Aspergillus, Fusarium, Humicola, Mucor, Myceliophthora, Neurospora, Penicillium, Thielavia, Tolypocladium, and Trichoderma cells, preferably Fusarium venenatum, Aspergillus niger, or Aspergillus oryzae. The method of the invention is useful for monitoring the expression of a plurality of genes in filamentous fungal cells, in order to improve the cells' protein production capacity when such organisms are used for the industrial production of proteins (e.g., enzymes). Sequences ADU55289-ADU55894 represent ESTs derived from Aspergillus niger strain Bo-95 which were obtained in an example of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?docID=US20040222367.		
XX			
SQ	Sequence 1024 BP; 275 A; 204 C; 275 G; 269 T; 0 U; 1 Other;		

Query Match 81.7%; Score 18.8; DB 13; Length 1024;  
Best Local Similarity 90.9%; Pred. No. 59;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCACC 23  
    |||||  
Db 57 CGTTAAGTTATTATGATTCACC 36

Search completed: January 9, 2006, 18:38:56  
Job time : 329 secs





(Atlanta, Georgia). Poly A+ RNA was separated from total C. parvum RNA using the Poly(A) Quik mRNA Isolation Kit from Stratagene. Directional cDNA was synthesized by first-strand priming with a Xho I-oligo d(T) linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the unamplified library was >95% recombinant and contained 3.8 X 10(6) independent clones. PCR analysis of 20 random clones indicated that the average insert size was ca. 1.1 kb."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23  
|||||  
Db 227 CCGTAAAGTTATTATGAGTCACC 205

RESULT 2

AA167899/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

AA167899 427 bp mRNA linear EST 23-AUG-2000  
CpEST.044 unizAPcPIOWAsporoLib1 Cryptosporidium parvum cDNA 5',  
similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA  
sequence.

AA167899  
AA167899.1 GI:1746067  
EST.  
Cryptosporidium parvum  
Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 427)  
Strong,W.B. and Nelson,R.G.  
Preliminary profile of the Cryptosporidium parvum genome: an  
expressed sequence tag and genome survey sequence analysis  
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)  
10717299

Contact: Nelson, R. G.  
Depts. of Medicine & Pharmaceutical Chemistry  
San Francisco General Hospital-University of California, San  
Francisco  
Box 0811, San Francisco, CA 94143-0811, USA  
Tel: 415 206 8846  
Fax: 415 206 3353  
Email: malaria@itsa.ucsf.edu

Submitted sequence has been edited to remove vector sequences 5' to  
the insert, to correct miscalled bases and assign uncalled (N)  
bases throughout the sequence, and to terminate when base-calling  
became ambiguous.

Seq primer: M13 reverse  
High quality sequence stop: 427.

FEATURES

source

Location/Qualifiers  
1. .427  
/organism="Cryptosporidium parvum"  
/mol\_type="mRNA"  
/strain="IOWA"  
/db\_xref="taxon:5807"  
/dev\_stage="sporozoite"  
/lab\_host="E. coli XL1 Blue MRF' Kan"  
/clone\_lib="unizAPcPIOWAsporoLib1"

/note="Vector: UnizAP XR; Site 1: EcoR I; Site 2: Xho I;  
Total RNA was isolated from purified Cryptosporidium  
parvum sporozoites using TRIzol reagent (GIBCO-BRL).  
Directional cDNA was synthesized by first-strand priming  
with a Xho I-oligo d(T) linker-primer, second-stranding  
with RNase H and DNA polymerase I, ligation of EcoR I  
linkers, and digestion with Xho I, all using the  
Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned

into the EcoR I and Xho I sites of Lambda Uni-ZAP XR  
vector; the primary library was >97% recombinant and  
contained 1.3 X 10(6) independent clones with an ca.  
average insert size of 1.3 kb. Based on open reading frame  
(orf) analysis of the first 64 sequence tags we estimate  
that up to one-third of the library is composed of genomic  
DNA clones since approximately 15% of the orfs were  
incorrectly oriented on the antisense strand."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 427;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23  
|||||  
Db 235 CCGTAAAGTTATTATGAGTCACC 213

RESULT 3

AA167914/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

AA167914 461 bp mRNA linear EST 23-AUG-2000  
CpEST.013 unizAPcPIOWAsporoLib1 Cryptosporidium parvum cDNA 5',  
similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA  
sequence.

AA167914  
AA167914.1 GI:1746082  
EST.  
Cryptosporidium parvum  
Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 461)  
Strong,W.B. and Nelson,R.G.  
Preliminary profile of the Cryptosporidium parvum genome: an  
expressed sequence tag and genome survey sequence analysis  
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)  
10717299

Contact: Nelson, R. G.  
Depts. of Medicine & Pharmaceutical Chemistry  
San Francisco General Hospital-University of California, San  
Francisco  
Box 0811, San Francisco, CA 94143-0811, USA  
Tel: 415 206 8846  
Fax: 415 206 3353  
Email: malaria@itsa.ucsf.edu

Submitted sequence has been edited to remove vector sequences 5' to  
the insert, to correct miscalled bases and assign uncalled (N)  
bases throughout the sequence, and to terminate when base-calling  
became ambiguous.

Seq primer: M13 reverse  
High quality sequence stop: 461.

FEATURES

source

Location/Qualifiers  
1. .461  
/organism="Cryptosporidium parvum"  
/mol\_type="mRNA"  
/strain="IOWA"  
/db\_xref="taxon:5807"  
/dev\_stage="sporozoite"  
/lab\_host="E. coli XL1 Blue MRF' Kan"  
/clone\_lib="unizAPcPIOWAsporoLib1"

/note="Vector: UnizAP XR; Site 1: EcoR I; Site 2: Xho I;  
Total RNA was isolated from purified Cryptosporidium  
parvum sporozoites using TRIzol reagent (GIBCO-BRL).  
Directional cDNA was synthesized by first-strand priming  
with a Xho I-oligo d(T) linker-primer, second-stranding  
with RNase H and DNA polymerase I, ligation of EcoR I  
linkers, and digestion with Xho I, all using the  
Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned  
into the EcoR I and Xho I sites of Lambda Uni-ZAP XR  
vector; the primary library was >97% recombinant and  
contained 1.3 X 10(6) independent clones with an ca.  
average insert size of 1.3 kb. Based on open reading frame

(orf) analysis of the first 64 sequence tags we estimate that up to one-third of the library is composed of genomic DNA clones since approximately 15% of the orfs were incorrectly oriented on the antisense strand."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 461;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23  
|||||  
Db 233 CCGTAAAGTTATTATGAGTCACC 211

RESULT 4

AA167900/c

LOCUS

DEFINITION

AA167900 485 bp mRNA linear EST 23-AUG-2000

CpEST.045 unizAPCpIOWAsporoLib1 Cryptosporidium parvum cDNA 5' similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Cryptosporidium parvum

Cryptosporidium parvum

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporidiidae; Cryptosporidium.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

1 (bases 1 to 485)

Strong,W.B. and Nelson,R.G.

Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis

Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)

10717299

Contact: Nelson, R. G.

Depts. of Medicine & Pharmaceutical Chemistry

San Francisco General Hospital-University of California, San Francisco

Box 0811, San Francisco, CA 94143-0811, USA

Tel: 415 206 8846

Fax: 415 206 3353

Email: malaria@itsa.ucsf.edu

Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.

Seq primer: M13 reverse

High quality sequence stop: 485.

FEATURES

source

Location/Qualifiers

1. .485

/organism="Cryptosporidium parvum"

/mol\_type="mRNA"

/strain="IOWA"

/db\_xref="taxon:5807"

/dev\_stage="sporozoite"

/lab\_host="E. coli XL1 Blue MRF' Kan"

/clone\_lib="unizAPCpIOWAsporoLib1"

/note="Vector: UniZAP XR; Site\_1: EcoR I; Site\_2: Xho I; Total RNA was isolated from purified Cryptosporidium parvum sporozoites using TRIZOL reagent (GIBCO-BRL). Directional cDNA was synthesized by first-strand priming with a Xho I-oligo d(T) linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the primary library was >97% recombinant and contained 1.3 X 10(6) independent clones with an ca. average insert size of 1.3 kb. Based on open reading frame (orf) analysis of the first 64 sequence tags we estimate that up to one-third of the library is composed of genomic DNA clones since approximately 15% of the orfs were incorrectly oriented on the antisense strand."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 485;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23  
|||||  
Db 216 CCGTAAAGTTATTATGAGTCACC 194

RESULT 5

AA167911/c

LOCUS

DEFINITION

AA167911 520 bp mRNA linear EST 23-AUG-2000

CpEST.003 unizAPCpIOWAsporoLib1 Cryptosporidium parvum cDNA 5' similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Cryptosporidium parvum

Cryptosporidium parvum

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporidiidae; Cryptosporidium.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

1 (bases 1 to 520)

Strong,W.B. and Nelson,R.G.

Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis

Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)

10717299

Contact: Nelson, R. G.

Depts. of Medicine & Pharmaceutical Chemistry

San Francisco General Hospital-University of California, San Francisco

Box 0811, San Francisco, CA 94143-0811, USA

Tel: 415 206 8846

Fax: 415 206 3353

Email: malaria@itsa.ucsf.edu

Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.

Seq primer: M13 reverse

High quality sequence stop: 520.

FEATURES

source

Location/Qualifiers

1. .520

/organism="Cryptosporidium parvum"

/mol\_type="mRNA"

/strain="IOWA"

/db\_xref="taxon:5807"

/dev\_stage="sporozoite"

/lab\_host="E. coli XL1 Blue MRF' Kan"

/clone\_lib="unizAPCpIOWAsporoLib1"

/note="Vector: UniZAP XR; Site\_1: EcoR I; Site\_2: Xho I; Total RNA was isolated from purified Cryptosporidium parvum sporozoites using TRIZOL reagent (GIBCO-BRL). Directional cDNA was synthesized by first-strand priming with a Xho I-oligo d(T) linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the primary library was >97% recombinant and contained 1.3 X 10(6) independent clones with an ca. average insert size of 1.3 kb. Based on open reading frame (orf) analysis of the first 64 sequence tags we estimate that up to one-third of the library is composed of genomic DNA clones since approximately 15% of the orfs were incorrectly oriented on the antisense strand."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 520;  
Best Local Similarity 100.0%; Pred. No. 3;







RESULT 11  
CA685630/c  
LOCUS  
DEFINITION CA685630 539 bp mRNA linear EST 25-NOV-2002  
wlm96.pk030.j22 wlm96 Triticum aestivum cDNA clone wlm96.pk030.j22  
5' end, mRNA sequence.  
ACCESSION CA685630  
VERSION CA685630.1 GI:25274269  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 539)  
AUTHORS Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,  
Miao,G., Caraher,N. and Hanafey,M.K.  
TITLE DuPont Wheat cDNA Sequence  
JOURNAL Unpublished (2002)  
COMMENT Contact: Scott V. Tingey  
Crop Genetics  
E. I. DuPont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: M13.  
FEATURES  
source Location/Qualifiers  
1..539  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Stephens"  
/db\_xref="taxon:4565"  
/clone="wlm96.pk030.j22"  
/tissue type="leaf"  
/clone\_lib="wlm96"  
/note="Vector: pBluescript SK+; Site\_1: EcoRI; Site\_2:  
XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after  
inoculation w/ E. graminis"

ORIGIN  
Query Match 88.7%; Score 20.4; DB 6; Length 539;  
Best Local Similarity 95.5%; Pred. No. 54;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
||| ||||||||||||||||  
Db 268 CGTTAAGTTATTATGAGTCACC 247

RESULT 12  
AU066519  
LOCUS  
DEFINITION AU066519 907 bp mRNA linear EST 04-AUG-2000  
AU066519 Chlamydomonas sp. HS-5 lambda ZAP II Chlamydomonas sp.  
HS-5 cDNA clone NaEX96-67, mRNA sequence.  
ACCESSION AU066519  
VERSION AU066519.1 GI:6448304  
KEYWORDS EST.  
SOURCE Chlamydomonas sp. HS-5  
ORGANISM Chlamydomonas sp. HS-5  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;  
Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.  
REFERENCE 1 (bases 1 to 907)  
AUTHORS Miyasaka,H., Kanaboshi,H. and Ikeda,K.  
TITLE Isolation of several anti-stress genes from halotolerant green alga  
Chlamydomonas by a simple functional expression screening in E.coli  
JOURNAL Unpublished (1999)  
COMMENT Contact: Kazunori Ikeda  
Environmental Symbiosis section  
Kansai Environmental Engineering Center Co.Ltd  
3-5 Adzuchimachi 1-Chome Chuo-ku, Osaka, Osaka 541-0052, Japan  
Email: daike@mb.infoweb.ne.jp  
NaCl inducible;  
Present address: The Kansai Electric Power Co.,Technical Research

Center, Bio-Laboratory; Nakoji 3-Chome 11-20, Amagasaki, Hyogo  
661-0974, Japan.  
FEATURES  
source Location/Qualifiers  
1..907  
/organism="Chlamydomonas sp. HS-5"  
/mol\_type="mRNA"  
/strain="HS-5"  
/db\_xref="taxon:108458"  
/clone="NaEX96-67"  
/clone\_lib="Chlamydomonas sp. HS-5 lambda ZAP II"  
/note="Vector: lambda ZAP II; The cDNA clone was isolated  
from the halotolerant green alga Chlamydomonas HS-5 by a  
functional expression screening in E.coli cells. The  
principle of the screening method was based on the  
acquisition of stress tolerance of the bacterial cells  
carrying the cDNA."  
ORIGIN  
Query Match 88.7%; Score 20.4; DB 1; Length 907;  
Best Local Similarity 95.5%; Pred. No. 57;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
||| ||||||||||||||||  
Db 677 CGTGAAGTTATTATGAGTCACC 698

RESULT 13  
BE430105  
LOCUS  
DEFINITION BE430105 558 bp mRNA linear EST 26-JUL-2000  
TAS007.B02R990628 ITEC TAS Wheat cDNA Library Triticum aestivum  
cDNA clone TAS007.B02, mRNA sequence.  
ACCESSION BE430105  
VERSION BE430105.1 GI:9427948  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 558)  
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,  
Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,  
Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,  
Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,  
Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,  
Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.  
TITLE International Triticeae EST Cooperative (ITEC): Production of  
Expressed Sequence Tags for Species of the Triticeae  
JOURNAL Unpublished (2000)  
COMMENT Contact: Selvaraj G  
Plant Biotechnology Institute, National Research Council of Canada  
110 Gymnasium Place, Saskatoon, SK S7N 0W9 Canada  
Tel: 306 975 5577  
Fax: 306 975 4839  
Email: Gopalan.Selvaraj@nrc.ca  
International Triticeae EST Cooperative (ITEC)  
http://wheat.pw.usda.gov/genome.  
FEATURES  
source Location/Qualifiers  
1..558  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone="TAS007.B02"  
/clone\_lib="ITEC TAS Wheat cDNA Library"

ORIGIN  
Query Match 86.1%; Score 19.8; DB 2; Length 558;  
Best Local Similarity 91.3%; Pred. No. 1e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23  
||||||| ||||| ||||| |||||



Db 346 CCGTAAAGTTATCATGAATCACC 368

RESULT 14  
DR045104/c  
LOCUS  
DEFINITION  
FP-7 G03.SEQ cDNA library of sporulating Phaeosphaeria nodorum SN15 on Wheat cv. Amery Triticum aestivum/Phaeosphaeria nodorum mixed EST library cDNA, mRNA sequence.

ACCESSION  
DR045104  
VERSION  
DR045104.1 GI:66908940  
KEYWORDS  
EST.  
SOURCE  
Triticum aestivum/Phaeosphaeria nodorum mixed EST library  
ORGANISM  
Triticum aestivum/Phaeosphaeria nodorum mixed EST library  
Eukaryota; mixed EST libraries.  
1 (bases 1 to 769)  
Lowe,R.G.T. and Oliver,R.P.  
AUTHORS  
Sporulation of Phaeosphaeria nodorum SN15  
JOURNAL  
Unpublished (2005)  
COMMENT  
Contact: Richard Oliver  
Austrian Centre for Necrotrophic Fungal Pathogens (ACNFP)  
Murdoch University  
South Street, Murdoch, W.A 6150, Australia  
Tel: +0893607404  
Email: roliver@murdoch.edu.au.

FEATURES  
source  
1..769  
/organism="Triticum aestivum/Phaeosphaeria nodorum mixed EST library"  
/mol\_type="mRNA"  
/db\_xref="taxon:331356"  
/dev\_stage="Sporulation"  
/clone\_lib="cDNA library of sporulating Phaeosphaeria nodorum SN15 on Wheat cv. Amery"  
/note="Vector: pTriplex2; Total RNA was extracted from P. nodorum strain SN15 infected wheat cv. Amery at 14 dpi. Library contains both fungal and plant sequences."

ORIGIN  
Query Match 86.1%; Score 19.8; DB 8; Length 769;  
Best Local Similarity 91.3%; Pred. No. 1.1e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTTATGAGTCACC 23  
|||||

Db 265 CCGTAAAGTTATCATGAATCACC 243  
|||||

RESULT 15  
DN476855/c  
LOCUS  
DEFINITION  
DN476855 771 bp mRNA linear EST 09-MAR-2005  
altr212xell A. brassicicola mycelial culture grown under conditions of Nitrogen Starvation Alternaria brassicicola cDNA clone altr212xell, mRNA sequence.

ACCESSION  
DN476855  
VERSION  
DN476855.1 GI:60674166  
KEYWORDS  
EST.  
SOURCE  
Alternaria brassicicola  
ORGANISM  
Alternaria brassicicola  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.  
1 (bases 1 to 771)  
Cramer,R.A., Craven,K.D., Thon,M.R., Cho,Y., Knudson,D.L., Mitchell,T.K. and Lawrence,C.B.  
AUTHORS  
Expressed Sequence Tag (EST) Analysis of a Compatible Alternaria brassicicola-Brassica oleracea Interaction  
JOURNAL  
Unpublished (2005)  
COMMENT  
Contact: Dr. Thomas K. Mitchell  
Center for Integrated Fungal Research, NC State University  
851 Main Campus Dr. Suite 233, Raleigh, NC 27606, USA  
Tel: (919) 513-3926  
Fax: (919) 513-0024  
Email: thomas\_mitchell@ncsu.edu

Seq primer: T7 SP6 primer.  
Location/Qualifiers  
1..771  
/organism="Alternaria brassicicola"  
/mol\_type="mRNA"  
/strain="ATCC 96866"  
/db\_xref="taxon:29001"  
/clone="altr212xell"  
/dev\_stage="mycelia"  
/clone\_lib="A. brassicicola mycelial culture grown under conditions of Nitrogen Starvation"  
/note="Vector: pGEMT; Mycelial culture grown under conditions of Nitrogen Starvation."

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Query Match 86.1%; Score 19.8; DB 8; Length 771;  
Best Local Similarity 91.3%; Pred. No. 1.1e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTTATGAGTCACC 23  
|||||

Db 238 CCGTAAAGTTATCATGAATCACC 216  
|||||

Search completed: January 9, 2006, 21:16:57  
Job time : 2476 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 18:17:01 ; Search time 102.5 Seconds  
(without alignments)  
398.867 Million cell updates/sec

Title: US-09-954-586-59  
Perfect score: 23  
Sequence: 1 ccgtaaagtattatgagtcacc 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*  
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8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23	100.0	1750	3 US-08-949-770-1	Sequence 1, Appli
C 2	18.8	81.7	439	2 US-08-093-144-3	Sequence 3, Appli
C 3	18.8	81.7	444	2 US-08-093-144-6	Sequence 6, Appli
C 4	18.8	81.7	446	2 US-08-093-144-4	Sequence 4, Appli
C 5	18.8	81.7	568	3 US-09-533-559-4068	Sequence 4068, Ap
C 6	18.8	81.7	1024	3 US-09-533-559-3839	Sequence 3839, Ap
C 7	18.8	81.7	2055	3 US-10-121-740-3	Sequence 3, Appli
C 8	18.8	81.7	2089	3 US-10-121-740-1	Sequence 1, Appli
C 9	18.2	79.1	709	3 US-08-998-416-281	Sequence 281, App
C 10	17.8	77.4	1102	3 US-10-037-417-43	Sequence 43, Appl
C 11	17.8	77.4	1102	3 US-10-037-417-45	Sequence 45, Appl
C 12	17.4	75.7	601	3 US-09-949-016-121653	Sequence 121653,
C 13	17.4	75.7	601	3 US-09-949-016-121654	Sequence 121654,
C 14	17.4	75.7	601	3 US-09-949-016-165267	Sequence 165267,
C 15	17.4	75.7	601	3 US-09-949-016-165268	Sequence 165268,
C 16	17.4	75.7	35262	3 US-09-949-016-12797	Sequence 12797, A
C 17	17.4	75.7	35263	3 US-09-949-016-16399	Sequence 16399, A
C 18	17.4	75.7	69737	3 US-09-949-016-15140	Sequence 15140, A
C 19	17.2	74.8	444	2 US-08-093-144-5	Sequence 5, Appli
C 20	17.2	74.8	703	3 US-08-998-416-178	Sequence 178, App
C 21	17.2	74.8	723	3 US-08-998-416-952	Sequence 952, App
C 22	17.2	74.8	1665	3 US-09-805-127-7	Sequence 7, Appli
C 23	17.2	74.8	1776	3 US-09-350-710B-1	Sequence 1, Appli
C 24	17.2	74.8	1788	2 US-08-867-820A-1	Sequence 1, Appli

C 25	16.8	73.0	92505	3 US-09-949-016-14018	Sequence 14018, A
C 26	16.8	73.0	130971	3 US-09-949-016-14205	Sequence 14205, A
C 27	16.6	72.2	409	3 US-09-265-585C-79	Sequence 79, Appl
C 28	16.6	72.2	1279	3 US-09-186-276B-45	Sequence 45, Appl
C 29	16.6	72.2	1279	3 US-08-842-445-45	Sequence 45, Appl
C 30	16.6	72.2	1279	3 US-09-186-188B-45	Sequence 45, Appl
C 31	16.6	72.2	1279	3 US-09-265-585C-45	Sequence 45, Appl
C 32	16.6	72.2	139562	3 US-09-949-016-13451	Sequence 13451, A
C 33	16.4	71.3	601	3 US-09-949-016-157835	Sequence 157835,
C 34	16.4	71.3	191433	3 US-09-949-016-16144	Sequence 16144, A
C 35	16.2	70.4	601	3 US-09-949-016-141451	Sequence 141451,
C 36	16.2	70.4	601	3 US-09-949-016-141452	Sequence 141452,
C 37	16.2	70.4	601	3 US-09-949-016-141453	Sequence 141453,
C 38	16.2	70.4	2059	3 US-09-489-847-119	Sequence 119, App
C 39	16.2	70.4	2076	3 US-09-489-847-51	Sequence 51, Appl
C 40	16.2	70.4	22846	2 US-08-469-461-3	Sequence 3, Appli
C 41	16.2	70.4	22846	3 US-07-890-609-3	Sequence 16312, A
C 42	16.2	70.4	25122	3 US-09-949-016-16312	Sequence 11820, A
C 43	16.2	70.4	192700	3 US-09-949-016-11820	Sequence 17182, A
C 44	16.2	70.4	192704	3 US-09-949-016-17182	Sequence 15753, A
C 45	16.2	70.4	236964	3 US-09-949-016-15753	

ALIGNMENTS

RESULT 1  
US-08-949-770-1/c  
; Sequence 1, Application US/08949770  
; Patent No. 6063604  
; GENERAL INFORMATION:  
; APPLICANT: Wick, James F.  
; APPLICANT: Mueller, Reinhold  
; APPLICANT: Blassak, Michele  
; APPLICANT: Wilkosz, Richard K.  
; TITLE OF INVENTION: Target Nucleic Acid Sequence Amplification  
; Patent No. 6063604  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/949,770  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/617,045  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pochopien, Donald J.  
; REGISTRATION NUMBER: 32,167  
; REFERENCE/DOCKET NUMBER: 28003/33045  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1750 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:

; NAME/KEY: misc feature
; OTHER INFORMATION: /= "18s rRNA gene of Cryptosporidium
; OTHER INFORMATION: parvum"
US-08-949-770-1

Query Match 100.0%; Score 23; DB 3; Length 1750;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
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Db 254 CCGTAAAGTTATTATGAGTCACC 232

RESULT 2
US-08-093-144-3/c
; Sequence 3, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-3

Query Match 81.7%; Score 18.8; DB 2; Length 439;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
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Db 156 CGAAAGTTATTATGAATCACC 135

RESULT 3
US-08-093-144-6/c
; Sequence 6, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:

; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-6

Query Match 81.7%; Score 18.8; DB 2; Length 444;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
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Db 156 CGAAAGTTATTATGAATCACC 135

RESULT 4
US-08-093-144-4/c
; Sequence 4, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144

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; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,192  
; FILING DATE: 15-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hymo, Lawrence A.  
; REGISTRATION NUMBER: 19,057  
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 446 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-093-144-4

Query Match 81.7%; Score 18.8; DB 2; Length 446;  
Best Local Similarity 90.9%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
Db 158 CGAAAAGTTATTATGAATCACC 137

RESULT 5  
US-09-533-559-4068/c  
; Sequence 4068, Application US/09533559  
; Patent No. 6902887  
; GENERAL INFORMATION:  
; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjørke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: 5849.200-US  
; CURRENT APPLICATION NUMBER: US/09/533,559  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 09/273,623  
; EARLIER FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4068  
; LENGTH: 568  
; TYPE: DNA  
; ORGANISM: Aspergillus niger  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(568)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-533-559-4068

Query Match 81.7%; Score 18.8; DB 3; Length 568;  
Best Local Similarity 90.9%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
Db 249 CGTTAAGTTATTATGATTCACC 228

RESULT 6  
US-09-533-559-3839/c  
; Sequence 3839, Application US/09533559  
; Patent No. 6902887

; GENERAL INFORMATION:  
; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjørke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: 5849.200-US  
; CURRENT APPLICATION NUMBER: US/09/533,559  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 09/273,623  
; EARLIER FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3839  
; LENGTH: 1024  
; TYPE: DNA  
; ORGANISM: Aspergillus niger  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1024)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-533-559-3839

Query Match 81.7%; Score 18.8; DB 3; Length 1024;  
Best Local Similarity 90.9%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
Db 57 CGTTAAGTTATTATGATTCACC 36

RESULT 7  
US-10-121-740-3/c  
; Sequence 3, Application US/10121740  
; Patent No. 6911338  
; GENERAL INFORMATION:  
; APPLICANT: Strobel, Gary  
; APPLICANT: Manker, Denise  
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
; TITLE OF INVENTION: USE  
; FILE REFERENCE: AQ 2019.40  
; CURRENT APPLICATION NUMBER: US/10/121,740  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 60/283,902  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/363,072  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2055  
; TYPE: DNA  
; ORGANISM: Muscodor roseus  
US-10-121-740-3

Query Match 81.7%; Score 18.8; DB 3; Length 2055;  
Best Local Similarity 90.9%; Pred. No. 18;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23  
Db 245 CGTGAAGTTATTATGAATCACC 224

RESULT 8  
US-10-121-740-1/c  
; Sequence 1, Application US/10121740  
; Patent No. 6911338  
; GENERAL INFORMATION:

; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2089
; TYPE: DNA
; ORGANISM: Muscodor albus
US-10-121-740-1

Query Match 81.7%; Score 18.8; DB 3; Length 2089;
Best Local Similarity 90.9%; Pred. No.18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
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Db 258 CGTGAAGTTATTATGAATCACC 237

RESULT 9
US-08-998-416-281
; Sequence 281, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jorgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1237UP
US-08-998-416-281
Query Match 79.1%; Score 18.2; DB 3; Length 709;
Best Local Similarity 87.0%; Pred. No.33;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCGTAAAGTTATTATGAGTCACC 23
||| ||||||||| |||||
Db 418 CCGAAAAGTTATTATGAATCATC 440
RESULT 10
US-10-037-417-43/C
; Sequence 43, Application US/10037417
; Patent No. 6903201
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 1102



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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-037-417-43

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Query Match          77.4%; Score 17.8; DB 3; Length 1102;
Best Local Similarity 90.5%; Pred. No. 51;
Matches 19: Conservative 0; Mismatches 2; Indels 0; Caps 0;

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**QY**

1 CCGTAAAGTTATTATGAGTCA 21  
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**D6**

92 CCGTAAAGTGAGTATGAGTCA 72

RESULT 11  
US-10-037-417-45/c  
; Sequence 45, Application US/10037417  
; Patent No. 6903201

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh

APPLICANT: Alsbrook II, John P

APPLICANT: Tchernev, Velizar T

APPLICANT: Liu, Xiaohong

APPLICANT: Spytek, Kimberly A

APPLICANT: Patturajan, Meera

APPLICANT: Grosse, William M

APPLICANT: Lepley, Denise M

APPLICANT: Burgess, Catherine E

APPLICANT: Vernet, Corine A.M.

APPLICANT: Li, Li

APPLICANT: Gorman, Linda

APPLICANT: Edinger, Shlomit R

APPLICANT: Sciore, Paul

APPLICANT: Ellerman, Karen

APPLICANT: Malyankar, Uriel M

APPLICANT: Rothenberg, Mark

APPLICANT: Stone, David J

APPLICANT: Boldog, Ferenc L

APPLICANT: Guo, Xiaojia

APPLICANT: Shenoy, Suresh G

APPLICANT: Anderson, David W

APPLICANT: Padigaru, Muralidhara

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Miller, Charles E

APPLICANT: Eisen, Andrew J

APPLICANT: EIBEN, ANDREW J.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-235

; CURRENT APPLICATION NUMBER: US/10/037,417

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/260,018  
 ; PRIOR FILING DATE: 2001-01-05

;  
: PRIOR FILING DATE: 2001-01-05  
: PRIOR APPLICATION NUMBER: 60/

;; PRIOR APPLICATION NUMBER: 80/280,360  
: PRIOR FILING DATE: 2001-01-08

;; PRIOR FILING DATE: 2001-01-08  
;; PRIOR APPLICATION NUMBER: 60/121,100

PRIOR FILING DATE: 2001-02-28

;; PRIOR APPLICATION NUMBER: 60/

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/

;; PRIOR FILING DATE: 2001-05-15  
: PRIOR APPLICATION NUMBER: 60/303,231

;  
; PRIOR APPLICATION NUMBER: 607  
; PRIOR FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 60/305,060

;  
; PRIOR FILING DATE: 2001-07-12

;; PRIOR APPLICATION NUMBER: 60/318,405

;  
PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/318,700

; PRIOR FILING DATE: 2001-09-12  
 ; NUMBER OF SEQ ID NOS: 327

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; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver 2.1

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; SOFTWARE: PALENCIA VER. 2.1
; SEO ID NO 45

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; SEQ ID NO 12
; LENGTH: 1102

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TYPE: DNA

ORGANISM: Homo sapiens

US-10-037-417-45

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Query Match          77.4%; Score 17.8; DB 3; Length 1102;
Best Local Similarity 90.5%; Pred. No. 51;
Matches 19: Conservative 0; Mismatches 2; Indels 0

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QY	1	CCGTAAAGTTATTATGAGTCA	21
pb	92	CCGTAAAGTGAGTATGAGTCA	72

RESULT 12  
US-09-949-016-121653/c  
; Sequence 121653, Application US/09949016  
; Patent No. 6812339

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; PATENT NO. 081253
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KN
; TITLE OF INVENTION: WITH HUMAN DISEASE
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,0
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4
; SEQ ID NO 121653
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-121653

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Query Match 75.7%; Score 17.4; DB 3; Length 601;  
Best Local Similarity 94.7%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 1; Indels

QY 4 TAAAGTTATTATGAGTCAC 22  
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Db 275 TAAAGTTAGTATGAGTCAC 257

RESULT 13  
US-09-949-016-121654/c  
; Sequence 121654, Application US/09949016  
; Patent No. 6812339

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/ PATENT NO: 0012355
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KN
/ TITLE OF INVENTION: WITH HUMAN DISEASE
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,0
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSEQ for Windows Version 4
/ SEQ ID NO 121654
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-121654

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Query Match	75.7%;	Score 17.4;	DB 3;	Length 601;
Best Local Similarity	94.7%;	Pred. No. 76;		
Matches 18:	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

US-10-037-417-45

Search completed: January 9, 2006, 21:20:29  
Job time : 103.5 secs

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QY      4 TAAAGTTATTATGAGTCAC 22
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Db     154 TAAAGTTAGTATGAGTCAC 136

RESULT 14
US-09-949-016-165267/c
; Sequence 165267, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165267
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-165267

Query Match      75.7%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. NO. 76;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TAAAGTTATTATGAGTCAC 22
      ||||| ||||| ||||| |||||
Db     154 TAAAGTTAGTATGAGTCAC 136

RESULT 15
US-09-949-016-165268/c
; Sequence 165268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165268
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-165268

Query Match      75.7%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. NO. 76;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      4 TAAAGTTATTATGAGTCAC 22
      ||||| ||||| ||||| |||||
Db     275 TAAAGTTAGTATGAGTCAC 257
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 19:55:45 ; Search time 517 Seconds  
(without alignments)  
367.883 Million cell updates/sec

Title: US-09-954-586-59  
Perfect score: 23  
Sequence: 1 ccgtaaagtattatgagtcacc 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:  
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3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
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8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23	100.0	23	3	US-09-954-695-47 Sequence 47, Appl
C 2	23	100.0	23	3	US-09-954-695-53 Sequence 53, Appl
C 3	23	100.0	23	3	US-09-954-695-59 Sequence 59, Appl
C 4	23	100.0	23	3	US-09-954-695-65 Sequence 65, Appl
C 5	23	100.0	23	3	US-09-954-586-47 Sequence 47, Appl
C 6	23	100.0	23	3	US-09-954-586-53 Sequence 53, Appl
C 7	23	100.0	23	3	US-09-954-586-59 Sequence 59, Appl
C 8	23	100.0	23	3	US-09-954-586-65 Sequence 65, Appl
C 9	18.8	81.7	568	8	US-10-653-047-4068 Sequence 4068, Ap
C 10	18.8	81.7	685	6	US-10-094-097B-112 Sequence 112, App
C 11	18.8	81.7	1024	8	US-10-653-047-3839 Sequence 3839, Ap
C 12	18.8	81.7	1228	9	US-10-483-439-1 Sequence 1, Appli
C 13	18.8	81.7	2055	6	US-10-121-740-3 Sequence 3, Appli
C 14	18.8	81.7	2055	7	US-10-623-432-3 Sequence 3, Appli
C 15	18.8	81.7	2055	10	US-11-131-659-3 Sequence 3, Appli
C 16	18.8	81.7	2089	6	US-10-121-740-1 Sequence 1, Appli
C 17	18.8	81.7	2089	7	US-10-623-432-1 Sequence 1, Appli
C 18	18.8	81.7	2089	10	US-11-131-659-1 Sequence 1, Appli
C 19	18.4	80.0	383	6	US-10-062-674-1363 Sequence 1363, Ap
C 20	18.4	80.0	1421	8	US-10-425-115-31251 Sequence 31251, A
C 21	17.8	77.4	1102	7	US-10-037-417-43 Sequence 43, Appl
C 22	17.8	77.4	1102	7	US-10-037-417-45 Sequence 45, Appl
C 23	17.2	74.8	526	4	US-09-925-065A-384347 Sequence 384347,

24	17.2	74.8	587	5	US-10-027-632-274162	Sequence 274162,
25	17.2	74.8	587	5	US-10-027-632-274163	Sequence 274163,
26	17.2	74.8	587	6	US-10-027-632-274162	Sequence 274162,
27	17.2	74.8	587	6	US-10-027-632-274163	Sequence 274163,
C 28	17.2	74.8	594	4	US-09-925-065A-248273	Sequence 248273,
C 29	17.2	74.8	632	4	US-09-925-065A-131139	Sequence 131139,
30	17.2	74.8	780	7	US-10-424-599-40289	Sequence 40289, A
C 31	17.2	74.8	1665	7	US-10-417-264-7	Sequence 7, Appli
C 32	17.2	74.8	1798	6	US-10-182-329-110	Sequence 110, App
C 33	17.2	74.8	1798	7	US-10-182-327-195	Sequence 195, App
C 34	17.2	74.8	1798	7	US-10-361-002-8	Sequence 8, Appli
C 35	17.2	74.8	1798	7	US-10-361-004-8	Sequence 8, Appli
36	17.2	74.8	3480	6	US-10-297-621-2	Sequence 2, Appli
37	16.8	73.0	361	6	US-10-062-674-1309	Sequence 1309, Ap
C 38	16.8	73.0	534	4	US-09-925-065A-610811	Sequence 610811,
C 39	16.8	73.0	569	4	US-09-925-065A-657517	Sequence 657517,
C 40	16.8	73.0	569	4	US-09-925-065A-657518	Sequence 657518,
41	16.8	73.0	596	5	US-10-027-632-223147	Sequence 223147,
42	16.8	73.0	596	6	US-10-027-632-223147	Sequence 223147,
43	16.8	73.0	598	5	US-10-027-632-216868	Sequence 216868,
44	16.8	73.0	598	5	US-10-027-632-216869	Sequence 216869,
45	16.8	73.0	598	6	US-10-027-632-216868	Sequence 216868,

ALIGNMENTS

RESULT 1  
US-09-954-695-47/c  
; Sequence 47, Application US/09954695  
; Patent No. US20020055116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-02.UT  
; CURRENT APPLICATION NUMBER: US/09/954,695  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 47  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-47  
Query Match 100.0%; Score 23; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCGTAAAGTTATTATGAGTCACC 23  
| | | | | | | | | | | | | | | | | | | | | |  
Db 23 CCGTAAAGTTATTATGAGTCACC 1  
RESULT 2  
US-09-954-695-53/c  
; Sequence 53, Application US/09954695  
; Patent No. US20020055116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-02.UT  
; CURRENT APPLICATION NUMBER: US/09/954,695

; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-53

Query Match 100.0%; Score 23; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23  
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Db 23 CCGTAAAGTTATTATGAGTCACC 1

RESULT 3

US-09-954-695-59  
; Sequence 59, Application US/09954695  
; Patent No. US20020055116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-02.UT  
; CURRENT APPLICATION NUMBER: US/09/954,695  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 59  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-59

Query Match 100.0%; Score 23; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23  
|||||  
Db 1 CCGTAAAGTTATTATGAGTCACC 23

RESULT 4

US-09-954-695-65  
; Sequence 65, Application US/09954695  
; Patent No. US20020055116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-02.UT  
; CURRENT APPLICATION NUMBER: US/09/954,695  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 65  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-65

Query Match 100.0%; Score 23; DB 3; Length 23;  
Best Local Similarity 69.6%; Pred. No. 1.2;  
Matches 16; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23  
|||||  
Db 1 CCGUAAAGUUAUUAUGAGUCACC 23

RESULT 5

US-09-954-586-47/c  
; Sequence 47, Application US/09954586  
; Patent No. US20020146717A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-03.UT  
; CURRENT APPLICATION NUMBER: US/09/954,586  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 47  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-586-47

Query Match 100.0%; Score 23; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23  
|||||  
Db 23 CCGTAAAGTTATTATGAGTCACC 1

RESULT 6

US-09-954-586-53/c  
; Sequence 53, Application US/09954586  
; Patent No. US20020146717A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-03.UT  
; CURRENT APPLICATION NUMBER: US/09/954,586  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

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; OTHER INFORMATION: Synthetic Construct
US-09-954-586-53

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGTAAAGTTATTATGAGTCACC 23
Db      23 CCGTAAAGTTATTATGAGTCACC 1

RESULT 7
US-09-954-586-59
; Sequence 59, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-59

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGTAAAGTTATTATGAGTCACC 23
Db      1 CCGTAAAGTTATTATGAGTCACC 23

RESULT 8
US-09-954-586-65
; Sequence 65, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-65

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 69.6%; Pred. No. 1.2;
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Matches 16; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGTAAAGTTATTATGAGTCACC 23
Db      1 CCGTAAAGTUUUAUGAGUCACC 23

RESULT 9
US-10-653-047-4068/c
; Sequence 4068, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4068
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(568)
; OTHER INFORMATION: n = A,T,C or G
US-10-653-047-4068

Query Match      81.7%; Score 18.8; DB 8; Length 568;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      249 CGTAAAGTTATTATGATTCACC 228

RESULT 10
US-10-094-097B-112/c
; Sequence 112, Application US/10094097B
; Publication No. US20030185840A1
; GENERAL INFORMATION:
; APPLICANT: IOANNIDES, CONSTANTIN G.
; APPLICANT: PEOPLES, JR., GEORGE E.
; TITLE OF INVENTION: INDUCTION OF TUMOR IMMUNITY BY VARIANTS OF FOLATE
; TITLE OF INVENTION: BINDING PROTEIN
; FILE REFERENCE: AH-P02120US1 / UTSC:686US
; CURRENT APPLICATION NUMBER: US/10/094,097B
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 10/094,097
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,676
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 685
; TYPE: DNA
; ORGANISM: Cladosporium fulvum
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (197)..(683)
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; OTHER INFORMATION: N = A, C, G, or T/U
US-10-094-097B-112

Query Match      81.7%; Score 18.8; DB 6; Length 685;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      249 CGTGAAGTTATTATGATTCACC 228

RESULT 11
US-10-653-047-3839/c
; Sequence 3839, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3839
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1024)
; OTHER INFORMATION: n = A,T,C or G
US-10-653-047-3839

Query Match      81.7%; Score 18.8; DB 8; Length 1024;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      57 CGTTAAGTTATTATGATTCACC 36

RESULT 12
US-10-483-439-1/c
; Sequence 1, Application US/10483439
; Publication No. US20050069999A1
; GENERAL INFORMATION:
; APPLICANT: Sharma, Sreenath V.
; APPLICANT: Matsushita, Noriko
; APPLICANT: Ando, Katsuhiko
; APPLICANT: Yoshida, Chitose
; APPLICANT: Nakano, Hirofumi
; APPLICANT: Agatsuma, Tsutomu
; APPLICANT: Kanda, Yutaka
; TITLE OF INVENTION: SH3 DOMAIN BINDING INHIBITORS
; FILE REFERENCE: 09859/020055-US0
; CURRENT APPLICATION NUMBER: US/10/483,439
; CURRENT FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: PCT/JP02/03932
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 1
; LENGTH: 1228
; TYPE: DNA
; ORGANISM: MPC1005
US-10-483-439-1

Query Match      81.7%; Score 18.8; DB 9; Length 1228;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      214 CGAAAAGTTATTATGAATCACC 193

RESULT 13
US-10-121-740-3/c
; Sequence 3, Application US/10121740
; Publication No. US20030186425A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-121-740-3

Query Match      81.7%; Score 18.8; DB 6; Length 2055;
Best Local Similarity 90.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      245 CGTGAAGTTATTATGAATCACC 224

RESULT 14
US-10-623-432-3/c
; Sequence 3, Application US/10623432
; Publication No. US20040141955A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/623,432
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US/10/121,740
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-623-432-3
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Query Match 81.7%; Score 18.8; DB 7; Length 2055;  
Best Local Similarity 90.9%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGATCACC 23  
||| ||||| ||||| ||||| |||||  
Db 245 CGTGAAGTTATTATGATCACC 224

RESULT 15  
US-11-131-659-3/c  
; Sequence 3, Application US/11131659  
; Publication No. US20050220769A1  
; GENERAL INFORMATION:  
; APPLICANT: Strobel, Gary  
; APPLICANT: Manker, Denise  
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
; TITLE OF INVENTION: USE  
; FILE REFERENCE: AQ 2019.40  
; CURRENT APPLICATION NUMBER: US/11/131,659  
; CURRENT FILING DATE: 2005-05-17  
; PRIOR APPLICATION NUMBER: US/10/121,740  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 60/283,902  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/363,072  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2055  
; TYPE: DNA  
; ORGANISM: Muscodor roseus  
US-11-131-659-3

Query Match 81.7%; Score 18.8; DB 10; Length 2055;  
Best Local Similarity 90.9%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGATCACC 23  
||| ||||| ||||| ||||| |||||  
Db 245 CGTGAAGTTATTATGATCACC 224

Search completed: January 10, 2006, 00:04:33  
Job time : 518 secs

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 21:17:07 ; Search time 215 Seconds  
(without alignments)  
77.993 Million cell updates/sec

Title: US-09-954-586-59  
Perfect score: 23  
Sequence: 1 ccgtaaagttattatgagtcacc 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:\*  
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10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.2	74.8	1732	6 US-10-519-379-1	Sequence 1, Appli
2	16.8	73.0	150437	7 US-11-112-908-44	Sequence 44, Appl
3	16.8	73.0	150491	7 US-11-112-908-46	Sequence 46, Appl
4	16.2	70.4	848	6 US-10-750-185-35778	Sequence 35778, A
5	16.2	70.4	848	6 US-10-750-623-35778	Sequence 35778, A
C 6	15.8	68.7	598	6 US-10-750-185-21192	Sequence 21192, A
C 7	15.8	68.7	598	6 US-10-750-623-21192	Sequence 21192, A
C 8	15.8	68.7	1077	6 US-10-750-185-49007	Sequence 49007, A
C 9	15.8	68.7	1077	6 US-10-750-623-49007	Sequence 49007, A
10	15.8	68.7	1433	6 US-10-750-185-27017	Sequence 27017, A
11	15.8	68.7	1433	6 US-10-750-623-27017	Sequence 27017, A
12	15.8	68.7	1459	6 US-10-750-185-48860	Sequence 48860, A
13	15.8	68.7	1459	6 US-10-750-623-48860	Sequence 48860, A
C 14	15.8	68.7	1836	6 US-10-750-185-63798	Sequence 63798, A
C 15	15.8	68.7	1836	6 US-10-750-623-63798	Sequence 63798, A
16	15.8	68.7	1842	6 US-10-750-185-56488	Sequence 56488, A
17	15.8	68.7	1842	6 US-10-750-623-56488	Sequence 56488, A
C 18	15.8	68.7	340000	7 US-11-102-978-3	Sequence 3, Appli
19	15.4	67.0	1841	6 US-10-750-185-54430	Sequence 54430, A
20	15.4	67.0	1841	6 US-10-750-623-54430	Sequence 54430, A
C 21	15.2	66.1	25	7 US-11-121-849-664285	Sequence 664285,
22	15.2	66.1	201	6 US-10-995-561-78246	Sequence 78246, A
C 23	15.2	66.1	853	6 US-10-750-185-54024	Sequence 54024, A

C 24	15.2	66.1	853	6 US-10-750-623-54024	Sequence 54024, A
25	15.2	66.1	950	6 US-10-957-569-43	Sequence 43, Appl
C 26	15.2	66.1	1085	6 US-10-750-185-44132	Sequence 44132, A
C 27	15.2	66.1	1085	6 US-10-750-623-44132	Sequence 44132, A
C 28	15.2	66.1	1193	6 US-10-750-185-26452	Sequence 26452, A
C 29	15.2	66.1	1193	6 US-10-750-623-26452	Sequence 26452, A
30	15.2	66.1	1861	7 US-11-192-374-2	Sequence 2, Appli
31	15.2	66.1	1956	6 US-10-750-185-45040	Sequence 45040, A
32	15.2	66.1	1956	6 US-10-750-623-45040	Sequence 45040, A
33	15.2	66.1	2241	7 US-11-192-374-1	Sequence 1, Appli
34	15.2	66.1	12152	7 US-11-124-368A-2929	Sequence 2929, Ap
35	15.2	66.1	29959	6 US-10-995-561-13475	Sequence 13475, A
36	15.2	66.1	43948	6 US-10-949-720-393	Sequence 393, App
37	15.2	66.1	90572	7 US-11-124-368A-2900	Sequence 2900, Ap
38	15.2	66.1	190882	7 US-11-121-086-69	Sequence 69, Appl
39	15	65.2	201	6 US-10-995-561-58799	Sequence 58799, A
C 40	15	65.2	396	6 US-10-769-744-492	Sequence 492, App
C 41	15	65.2	396	6 US-10-769-744-493	Sequence 493, App
C 42	15	65.2	396	6 US-10-769-744-494	Sequence 494, App
C 43	15	65.2	1627	6 US-10-750-185-29436	Sequence 29436, A
C 44	15	65.2	1627	6 US-10-750-623-29436	Sequence 29436, A
45	15	65.2	33042	6 US-10-995-561-13340	Sequence 13340, A

ALIGNMENTS

RESULT 1  
US-10-519-379-1/c  
; Sequence 1, Application US/10519379  
; Publication No. US20050255126A1  
; GENERAL INFORMATION:  
; APPLICANT: ASahi DENKA Co., Ltd.  
; TITLE OF INVENTION: New microorganism and method for producing aglucan by the new  
; TITLE OF INVENTION: microorganism  
; FILE REFERENCE: A0301  
; CURRENT APPLICATION NUMBER: US/10/519,379  
; CURRENT FILING DATE: 2004-12-27  
; NUMBER OF SEQ ID NOS: 4  
; SEQ ID NO 1  
; LENGTH: 1732  
; TYPE: DNA  
; ORGANISM: Aureobasidium pullulans ADK-34  
US-10-519-379-1

Query Match 74.8%; Score 17.2; DB 6; Length 1732;  
Best Local Similarity 86.4%; Pred. No. 60;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	2	CGTAAAGTTATTATGAGTCACC 23
Db	223	CGTTAGTTATTATGATCACC 202

RESULT 2  
US-11-112-908-44  
; Sequence 44, Application US/11112908  
; Publication No. US20050260659A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Cole  
; APPLICANT: Davis, Lisa M.  
; TITLE OF INVENTION: Breast Cancer Biomarkers  
; FILE REFERENCE: 04-164-US  
; CURRENT APPLICATION NUMBER: US/11/112,908  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/564,758  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/575,978  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US 60/631,702  
; PRIOR FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: US 60/633,826  
; PRIOR FILING DATE: 2004-12-07

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; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 150437
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-44

Query Match      73.0%; Score 16.8; DB 7; Length 150437;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CGTAAAGTTATTATGAGTCA 21
Db      122551 CATAAAGTTATTATGAGTTA 122570

RESULT 3
US-11-112-908-46
; Sequence 46, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 46
; LENGTH: 150491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-46

Query Match      73.0%; Score 16.8; DB 7; Length 150491;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CGTAAAGTTATTATGAGTCA 21
Db      59077 CATAAAGTTATTATGAGTTA 59096

RESULT 4
US-10-750-185-35778
; Sequence 35778, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21192
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-35778

Query Match      70.4%; Score 16.2; DB 6; Length 848;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CGTAAAGTTATTATGAGTCAC 22
Db      8 CGTAAATATTATGAACCAC 28

RESULT 5
US-10-750-623-35778
; Sequence 35778, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35778
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-35778

Query Match      70.4%; Score 16.2; DB 6; Length 848;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CGTAAAGTTATTATGAGTCAC 22
Db      8 CGTAAATATTATGAACCAC 28

RESULT 6
US-10-750-185-21192/c
; Sequence 21192, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21192
; LENGTH: 598
; TYPE: DNA
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; ORGANISM: Bovine MMBT01950  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(64)  
; OTHER INFORMATION: n is any nucleotide  
US-10-750-185-21192

Query Match 68.7%; Score 15.8; DB 6; Length 598;  
Best Local Similarity 81.0%; Pred. No. 2.4e+02;  
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCAC 22  
:|||||  
Db 531 YGTAAAGTTATTATTGTGAC 511

RESULT 7  
US-10-750-623-21192/c  
; Sequence 21192, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 21192  
; LENGTH: 598  
; TYPE: DNA  
; ORGANISM: Bovine MMBT01950  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(64)  
; OTHER INFORMATION: n is any nucleotide  
US-10-750-623-21192

Query Match 68.7%; Score 15.8; DB 6; Length 598;  
Best Local Similarity 81.0%; Pred. No. 2.4e+02;  
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCAC 22  
:|||||  
Db 531 YGTAAAGTTATTATTGTGAC 511

RESULT 8  
US-10-750-185-49007/c  
; Sequence 49007, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 49007  
; LENGTH: 1077  
; TYPE: DNA  
; ORGANISM: Bovine 19866880353038  
US-10-750-185-49007

Query Match 68.7%; Score 15.8; DB 6; Length 1077;  
Best Local Similarity 89.5%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTAAAGTTATTATGAGTCA 21  
:|||||  
Db 892 GTAAAGTTATTATAGTCA 874

RESULT 9  
US-10-750-623-49007/c  
; Sequence 49007, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 49007  
; LENGTH: 1077  
; TYPE: DNA  
; ORGANISM: Bovine 19866880353038  
US-10-750-623-49007

Query Match 68.7%; Score 15.8; DB 6; Length 1077;  
Best Local Similarity 89.5%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTAAAGTTATTATGAGTCA 21  
:|||||  
Db 892 GTAAAGTTATTATAGTCA 874

RESULT 10  
US-10-750-185-27017  
; Sequence 27017, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 27017

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;   LENGTH: 1433
;   TYPE: DNA
;   ORGANISM: Bovine 19866881858622
US-10-750-185-27017

Query Match      68.7%; Score 15.8; DB 6; Length 1433;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAAGTTATTATGAGTCACC 23
      ||||| ||||| ||||| |||||
Db      523 AAAGATATTATGACTCACC 541

RESULT 11
US-10-750-623-27017
; Sequence 27017, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 27017
; LENGTH: 1433
; TYPE: DNA
; ORGANISM: Bovine 19866881858622
US-10-750-623-27017

Query Match      68.7%; Score 15.8; DB 6; Length 1433;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAAGTTATTATGAGTCACC 23
      ||||| ||||| ||||| |||||
Db      523 AAAGATATTATGACTCACC 541

RESULT 12
US-10-750-185-48860
; Sequence 48860, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48860
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Bovine 19866880620497
US-10-750-185-48860

Query Match      68.7%; Score 15.8; DB 6; Length 1459;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAAGTTATTATGAGTCACC 23
      ||||| ||||| ||||| |||||
Db      709 AAAGTTATAATGAGTTACC 727

RESULT 13
US-10-750-623-48860
; Sequence 48860, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48860
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Bovine 19866880620497
US-10-750-623-48860

Query Match      68.7%; Score 15.8; DB 6; Length 1459;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAAGTTATTATGAGTCACC 23
      ||||| ||||| ||||| |||||
Db      709 AAAGTTATAATGAGTTACC 727

RESULT 14
US-10-750-185-63798/c
; Sequence 63798, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 63798
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Bovine 19866880348213
US-10-750-185-63798

Query Match      68.7%; Score 15.8; DB 6; Length 1836;
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```

US-10-750-185-48860

Query Match      68.7%; Score 15.8; DB 6; Length 1459;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAAGTTATTATGAGTCACC 23
      ||||| ||||| ||||| |||||
Db      709 AAAGTTATAATGAGTTACC 727

RESULT 13
US-10-750-623-48860
; Sequence 48860, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48860
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Bovine 19866880620497
US-10-750-623-48860

Query Match      68.7%; Score 15.8; DB 6; Length 1459;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAAGTTATTATGAGTCACC 23
      ||||| ||||| ||||| |||||
Db      709 AAAGTTATAATGAGTTACC 727

RESULT 14
US-10-750-185-63798/c
; Sequence 63798, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 63798
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Bovine 19866880348213
US-10-750-185-63798

Query Match      68.7%; Score 15.8; DB 6; Length 1836;
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Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TAAAGTTATTATGAGTCAC 22  
|||||  
Db 1221 TAAATATTATGACTCAC 1203

RESULT 15  
US-10-750-623-63798/c  
; Sequence 63798, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 63798  
; LENGTH: 1836  
; TYPE: DNA  
; ORGANISM: Bovine 19866880348213  
US-10-750-623-63798

Query Match 68.7%; Score 15.8; DB 6; Length 1836;  
Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TAAAGTTATTATGAGTCAC 22  
|||||  
Db 1221 TAAATATTATGACTCAC 1203

Search completed: January 10, 2006, 00:11:54  
Job time : 217 secs

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